

Query Match	25.0%;	Score	590.5;	DB	2;	Length	479;
Best Local Similarity	34.2%;	Pred. No.	4.4e-40;				
Matches	134;	Conservative	78;	Mismatches	155;	Indels	25;
Gaps							
QY	73	FXGIMFDAGSTGRVHVHFOFTRPPRTP-----TLTHETFKAVKPGLSAYADVVKSAQG	127				
Db	42	FTFIVIDAGSTGRGLHYFIHDPALASHGMPFKVEKIFQEVKPGLSFSAKSPSSAADS	101				
QY	128	IRELLDVAQKODIPDFFWKATPLVLKATAGLRLLPGEKAQLLKVKXE-VFKASPFVLVGDD	186				
Db	102	LEPLLQARKEVPHEFWKPTITLKATAGLRLLPGDMADDILLESVEERIFNSGFFAAFPD	161				
QY	187	CYSIMNGTDEGVSAMITINFLTGL-----KTPGGSSVGMLLDGGSTQIAFLPRV	237				
Db	162	AVNWPGSDGEGYSWFTNLILLETFTDPTVGHKPAHRSAAFDLGGSGTOLTYPNN	221				
QY	238	EGLTQASPPGYLTALRMFNRTKLYSYSVLGLGLMSARLAILGGVGQPAKDGEKVLSPC	297				
Db	222	EAVF-SEHVGVERDIDFGHHIRLTFSLGNGLAARLNIQLFEDNIEIESTHQLITSC	280				
QY	298	LSPSK-GEWEHAETVYRVSQGKAASLHELCAARVSEVLQ-NRVHRTVEVKHVDYAFS	355				
Db	281	MPEGYQLTEWEYALKFWNING--SSSHSPESCVCYGTTKNFVESSEIMHLRELKSPVWLES	338				
QY	356	YYIDLAAAGVLIDASKGSLVGDGFEIAAKYCRITLETQOSS-----PESCDMLTVV-SL	410				
Db	339	YFDDRALNSGLVKNEGKIEIURQFEAAEACRREKTEIDGSHMWPQCGLDTIYYSL	398				
QY	411	LQOEGFPRSKVLKLRKIDNVETSWALGAIF	442				
Db	399	LRDGYOFEDNOPLVLAKKIKGMEVSWGGLAF	410				

RESULT 2

T39109
probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39109
R;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21828
A;Accession: T39109
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-556 <BAR>
A;Cross-references: UNIPROT:Q9UT35; EMBL:AL121741; PIDN:CAB57338.1; GSPDB:GN000066; SPDB:
A;Experimental source: strain 972h-; cosmid c824
C;Genetics:
A;Gene: SPDB:SPAC824.08
A;Map position: 1

Query Match 21.5%; Score 508; DB 2; Length 556;
Best Local Similarity 32.4%; Pred. No. 2.8e-33;
Matches 142; Conservative 66; Mismatches 142; Indels 88; Gaps 17;
Qy 74 YGIMFDAGSTGTRVHFQFTRPREPTPLTHETKAVKPGLSAYADVDVEKSAQGIREDLD 133
Db 134 YLMIDAGSTGSRVHVVFQFN-CNPSPKLEEFPMIEPGLSSFAGDPEGAAASLDPLLD 192
Qy 134 VAKQDIPDFMKATPLVLKATAGLRLLPGEKAKLLQKVEVFKAS-PFLVGDDCVSIMN 192
Db 193 YAMENVEEYRRCSPIAVKATAGLRLTGESEAKILKSVRQHLNDYFPPIVKGVSTLE 252
Qy 193 GTDEGVSAWITINFLTGSLKTPGG-----SSVGMLDLGGSTQIAFLRVEVTLOASPPG- 247
Db 253 GSGMEGIWAMITINLLGTL--GGKATHSTVAVMDLGGASTQLVFEFPFASDGSVLVDG 309
Qy 248 YLTALRMFNRTYKLYSYLGLGLMSAR-----LAILGVGEGQPAKDG 290
Db 310 HKYVDLYNGEQYELYQHSGLYGLKEARKLHKFVNLNAAEKLSLELLG-----DS 361
Qy 291 KELVSPCL-----SPSKFGEWHAETTYRVSGOKAAASLHELCAARVSEVLQ----- 337
Db 362 TSIHPCLLNASLTHPDSKS--BASEVVF-VGFSLAHLSLQ--CRGIAEKALYDKNCP 416
Qy 338 -----NEVHR--TEEVKHVDVFAFSYYDLAAGVGLIDAEKGSLLVVGDFEIAAKVVC 388
Db 417 VRPCSFNGVHQPKFTETFTDSPILYLSFYDRMISLGM-----PSTFTIEDMKYLANSV 471
Qy 389 -----RTLETQPOSSPSPSCMDLTY-VSLLQLQEFGFPFRSKVLKTRKIDN 431
Db 472 SGPTYWQDAFSLTDALKELKEPE-----WCLLDNVMSLLSVGYEIPNNRQLHTAKIDN 527
Qy 432 VETSWALGAIFHYIDSUN 449
Db 528 KELGWCLGASLSMLSEQN 545

RESULT 3

A40732
guanosine-diphosphatase (EC 3.6.1.42) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YEL042w
C;Species: Saccharomyces cerevisiae
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A40732; B40732; S30837; S50502
R;Abelion, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.B.;
J. Cell Biol. 122, 307-323, 1993
A;Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylation
A;Reference number: A40732; MUID:93308137; PMID:8391537
A;Accession: A40732
A;Molecule type: DNA
A;Residues: 1-518 <ABE>
A;Cross-references: UNIPROT:P32621; EMBL:L19560; NID:g349392; PIDN:AAA34656.1; PID:g3493

A;Note: sequence extracted from NCBI backbone (NCBIN:134708, NCBI:P:134711)
A;Accession: B40732
A;Molecule type: protein
A;Residues: 125-144,238-257,276-281,366-374,399-412 <AB2>
R;Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor,
submitted to the EMBL Data Library, February 1993
A;Reference number: S30812
A;Accession: S30837

A;Molecule type: DNA
A;Residues: 1-518 <MUL>
A;Cross-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AAB65000.1; PID:g603637
R;Dietrich, F.S.
A;Description: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871.

A;Reference number: S50491

A;Accession: S50502

A;Molecule type: DNA

A;Residues: 1-518 <DIE>

A;Cross-references: EMBL:U18779; NID:g603625; PIDN:AAB65000.1; PID:g603637; MIPS:YEL042w

C;Genetics:

A;Gene: SGD:GDA1

A;Cross-references: SGD:S0000768; MIPS:YEL042w

A;Map position: 5L

C;Function:

A;Description: hydrolase

C;Superfamily: nucleoside triphosphatase chromatin-associated

C;Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein

F;10-24/Domain; transmembrane #status predicted <TM>

F;41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.1%; Score 498; DB 2; Length 518;
Best Local Similarity 33.1%; Pred. No. 1.7e-32;
Matches 144; Conservative 60; Mismatches 153; Indels 78; Gaps 15;

Qy 65 TAADGHEVFYGMFDAGSTGTRVHFQF--TRPREPTPLTHETKAVKPGLSAYADVD 121
Db 86 TCSSEHK--YVIMIDAGSTGSRVHIYKFDVCTSP-----PTLLDEKFDLMELGSLSFDTDS 139
Qy 122 EKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLLPGEKAKLLQKVE-VFKASP 180
Db 140 VGAANSLDPLLVKAMVYVPIKARSCTPVAVKATAGLRLGDAKSSKILSAVRDHLKDYD 199
Qy 181 F-LVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGS--SVGMLDLGGSTQIAFLPRV 237
Db 200 PPVVEGDSVIMNGDEGVSAWITINFLTGSLKTPGGS--SVGMLDLGGSTQIAFLPRV 259
Qy 238 EGTQASPPGVLTAALRMFNRTYKLYSYLGLGLMSARLAILGVGEGQPAKDGK----- 291
Db 260 PINKMDVGEHFKFDLKGDENTLYQFSLGYGLKEGNKVNVLVENALDKGKILKGDN 319
Qy 292 ----ELVSPCLSPSKFGEWE---HAETTYRV-----SGOKAAASLHELCAARVSEV 335
Db 320 TKTHQLSSPCLPPKVNATNEKVTLSEKETYIDFIDGPDPEPSGAQ-----CRFLTDEI 371
Qy 336 LQ-----NRVHRTVEVHV-----DFYAFSYYDLAAGVGLIDAEKGSLLVVD 379
Db 372 LNKDAQCCQSPSPFNGVHQPSLVRTFKESNDIYFYFYDRTRPLGM-----PLSFTLNE 426
Qy 380 FEIAAKVYCRLET-----QPOSSPSPSCMDLTY-VSLLQLQEFGFPFRSKVLK 425
Db 427 LNDLARIYCKGEETWNSVFSGIAGSLDESDSHFCLDSFQVSLHTGYDIPLORELRT 486
Qy 426 TRKIDNVETSWALGA 440
Db 487 GKTIANKKEIGWCLGA 501

RESULT 4

JC4616
apyrase (EC 3.6.1.5) precursor - potato
N;Alternate names: adenylypyrophosphatase; ATP-diphosphohydrolase
C;Species: Solanum tuberosum (potato)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C:Accession: JC4616; PC4147
R:Handa, M.; Guidotti, G.

Biochem. Biophys. Res. Commun. 218, 916-923, 1996

A:Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from *Populus euphratica*

A:Reference number: JC4616; MUID:96158985; PMID:8579614

A:Accession: JC4616

A:Molecule type: mRNA

A:Residues: 1-454 <HAN>

A:Cross-references: UNIPROT:P80595; NID:gl381632; PIDN:AA802720.1; PID:gl3816

A:Superfamily: nucleoside triphosphatase

A:Molecule type: protein

A:Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>

A:Experimental source: tubers

A:Note: The authors translated the codon GCA for residue 215 as Gly

C:Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydrolysis of ATP to ADP and inorganic phosphate. It has nucleotide substrate specificity, divalent cation requirement, and insensitivity to vanadate.

C:Genetics:

A:Gene: *iropl*

C:Superfamily: nucleoside triphosphatase chromatin-associated

C:Keywords: glycoprotein; hydrolase; transmembrane protein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:8-25/Domain: transmembrane #status predicted <TM>

F:31-454/Product: ATP-diphosphohydrolase #status predicted <TM>

F:44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding

F:192-212/Region: nucleotide binding #status predicted

F:192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding

F:192-212/Region: nucleotide binding #status predicted

F:390-410/Region: hydrophobic carboxyl end

F:151,262/Binding site: carbohydrate (Asn) #status predicted

Query Match 20.5%; Score 485; DB 2; Length 454;

Best Local Similarity 31.9%; Pred. No. 1.6e-31;

Matches 138; Conservative 68; Mismatches 183; Indels 44; Gaps 12;

QY 59 AHSPLGTADGHE-VFYGIMFDAGSTGRVHVQFTRPPETPTLTH-ETFAVKVPGLSA 116

Db 30 AQIPLRHLLSHSESHYAVIFDAGSTGRVHVQFTRPPETPTLTH-ETFAVKVPGLSA 116

QY 117 YADVDEKSAQGIREDLVAKQDIPDFWKATPLVLTAGLRLPGEKAQKLLQKVEVF 176

Db 90 YADDPKAANSLEPDLGAEVVPQELQSETPLELGATAGLRLPGEKAQKLLQKVEVF 176

QY 177 K-ASPFLLVGGDCVIMNGTDEGVSATINFLTGLSKTPGGSSVGMGLDGGSTQIAFLP 235

Db 150 KNQSTFHSKQDWITLDGTQSGSYMAAINVLLGNLGDYKSTATTIDLGGSSVGMGLDGGSTQIAFLP 235

QY 236 RVEGTQQA-----SPPGYLTALRMFNRTKLYSYVLGLMSARLAILGGVGGQPAKDGK 291

Db 210 SNEQFAKAPQNEDEGPYVQQHLSKDYNLVSHYSLYGLAGRAEIF-----KASR 261

QY 292 ELVSPCLSPSPKGEWEHAEVTVRSYGQKAAASLHLCARVSEVLQ-NRVHRTREVK--- 347

Db 262 NESPFALGEGCDGYSGYGVYKVPKPGSS-WKRCRLTRHALKINAKNIEECTPNG 320

QY 348 -----HVDFYAFSYYYDLAAGVGLIDAEKGGSLVVG-DFEIAAKYVCR----- 390

Db 321 VVNGGGGDKGKNIHASSFFYDGAQVGVDTKFPALAKPTQYLNAAKVAQCTNVADIKS 380

QY 391 --LETQSSSPSCMDLTY-VSLLLQEPFPRSKVLKTRKIDN-----VETSWALGAIFH 443

Db 381 IFPKTQDRNIPYLCMDLTYEYLLVDGFGFLNPKHEITVIHDVQYKNVYLVGAAPLGCDAID 440

QY 444 YIDSINRQKSPAS 456

Db 441 LVSSTTKIRVAS 453

RESULT 5

S48859

C:Species: Pisum sativum (garden pea)

C:Superfamily: nucleoside triphosphatase precursor, chromatin-associated - garden pea

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S65147; S48859
R:Hsieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.

Plant Mol. Biol. 30, 135-147, 1996

A:Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin-associated protein

A:Reference number: S65141; MUID:96197404; PMID:8616230

A:Accession: S65147

A:Molecule type: mRNA

A:Residues: 1-455 <HS2>

A:Cross-references: UNIPROT:P52914; EMBL:Z32743; NID:9563611; PIDN:CAA83655.1; PID:gs6361

A:Superfamily: nucleoside triphosphatase chromatin-associated

C:Keywords: nucleus

Query Match 18.7%; Score 442.5; DB 2; Length 455;

Best Local Similarity 29.2%; Pred. No. 4.6e-28;

Matches 125; Conservative 79; Mismatches 145; Indels 79; Gaps 15;

QY 74 YGIMFDAGSTGRVHVQFTRPPETPTLTH-----ETFAVKVPGLSAYADDOVEKSAQGI 128

Db 44 YAVVFDAGSTGRVHVQFTRPPETPTLTH-----NQNLDDLHLGKGVYNNKITPGLSSVANNPEQAQSL 99

QY 129 RELDVAKQDIPDFWKATPLVLTAGLRLPGEKAQKLLQKVEVF-KASPFLLVGGDC 187

Db 100 IPLLQAEADVVPDDLQPKTPVRLGATAGLRLNGDASEKILQSVRDMLSNRSTENVQPD 159

QY 188 VSIIMGTDEGVSATINFLTGLSKTPGGSSVGMGLDGGSTQIAF-----LPRVE 238

Db 160 VSIIDGTQEGSYLVVTVNVALGNLGGKVTGTGVIDLGGSSVGMGLDGGSTQIAF-----LPRVE 238

QY 239 GTLQASPPGYLTALRMFNRTKLYSYVLGLMSARLAILGGVGGQPAKDGKELVSPCL 298

Db 219 --ADGDDP-YIKKVVLGKIPYDLYVHSHFGREASRAELIKLTPRSP-----NPCL 267

QY 299 SPSPKGEWEHAEVTVRSYGQKAAASLHLCARVSEVLQNRVHRTREVKH----- 348

Db 268 LAGFNGIYTVSGEEFKATAYTSGANFNK-----CKNTIRKALKLNYPQYQNTCTFG 318

QY 349 -----VDFYAFSYYYDLAAGVGLIDAEKGGSLV-VGDFEIAAKYVCR-TLETQP 395

Db 319 GIWNGGGGNGKUNFASSTFFYPEDTGMVDASTFNFLRPVDIETKAKEACALNFEDAK 378

QY 396 QSSPF-----SCMDLTYVSLLLQEPFPRSKVLKLT--RKIDN-----VETSWALGA 440

Db 379 STYFPLDKKNVASYCNDLIIQYVLLVD-GFLDPLQKITSGKELEYQDAIVEAAWPLGN 437

QY 441 IFHVIDSL 448

Db 438 AVEAISAL 445

RESULT 6

G84442

probable nucleoside triphosphatase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: G84442

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Nuss, D.; Nietman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: G84442

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-516 <STO>

A:Cross-references: UNIPROT:O80612; GB:A802093; NID:g3461821; PIDN:AA032915.1; GSPDB:GM

C:Genetics:

A:Gene: At2g02970

A:Map position: 2

C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 15.7%; Score 372; DB 2; Length 516;

Best Local Similarity 29.0%; Pred. No. 3e-22;

C;Accession: T04439
R;Revan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Anzorge, W.; Bancroft, I.; Mewes, H.W. submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15359
A;Accession: T04439
A;Molecule type: DNA
A;Residues: 1-1052 <BEV>
A;Cross-references: UNIPROT:O49676; EMBL:AL021687
A;Experimental source: cultivar Columbia; EAC clone T18B16
C;Genetics:
A;Map position: 4
A;Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A;Note: T18B16.150

Query Match	10.4%;	Score 245.5;	DB 2;	Length 1052;
Best Local Similarity	25.3%;	Pred. No. 1.6e-11;		
Matches 116;	Conservative 60;	Mismatches 185;	Indels 97;	Gaps 20;
QY 55	WGQQAHS-----PLGTAADGHE-----	VFYGMFDAGSTGTRVHVFOQT 93		
Db				
483	WGQGSFSFEKSGSVNGTNPSTRKKLIRAVMIWVCLFLFAFLVIVTSITGRAYVYQAS 542			
QY 94	---RPPREPTLTHETFKAV-----	KPLSAYADDDVEKSAQAGIRELLDVAK 136		
Db				
543	INVKDSSLPVWKSUTEGISRSKRGRAYDRMETEPFGDKLVNNRTGLKTAIKPLIQWAE 602			
QY 137	QDIPDFWKATPLVLKATAGLRLLPGEKAQKLQKVEFKASPLVGGDDCVSIMNGTDE 196			
Db				
603	KQIPKNAHTTSLFVYATAGVRLRPADSSWILGNVWSILAKSPFTRCRREWKLISGTSE 662			
QY 197	GVSAIMITNPLTGS-LKTPGGSSVGMLDLGGGSTQIAFLPVEGTIQASPPGYLTALRMF 255			
Db				
663	AYFGWTALNYQTSMLGALPKKATFGALDLGSSSQVTF---EENERTHETNIN-LRIG 717			
QY 256	NRTYKLYSYSLGLGLMSA-----RLAILGVEGQPAKQK-ELVSPCLSPSPKGEWE 307			
Db				
718	SVNHHLSAYSLAGYGLNDAFDRSVVHLLAKPLPNVWKSLLIEGKLEMKHPCLNSGYNGQYI 777			
QY 308	HAETVYRVSGQAAASLHEL-----CAARVSE---VLQNRVHRTVEEVKHVDFYAF 354			
Db				
778	CSQCASSVQGKKKGKSGVSIKLVAPNWGECALAKNAPCALPDGYPR---PHGQFYAV 833			
QY 355	S-----YYDIAAGVGLIDA-EKGGSLVGVGFETAAKVVCRTLETQPOSSPF---SCMD 404			
Db				
834	SGGFVVYRPFNLISAEASLDVVLEKG-----REFCDKAWQVART-SVSPQ--PFIEQYCFR 885			
QY 405	LTYSVLLLQEFQFPKSVKULTRK---IDNVETSWALG 439			
Db				
886	APIYIVSLRE-----GLYITDKQIIIGSGSITWTLG 916			

RESULT 15
 C86276
 RA19.33 protein - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: C86276
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Hansen, N.F.; Hughes, B.; Huizuar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzio, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ter, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: C86276
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-508 <TO>
 A:Cross-references: UNIPROT:Q9X163; GB:AE005172; NID:G5080800; PIDN:AA039310.1; GSPDB:GN

```

C;Genetics:
A;Map position: 1
C;Superfamily: nucleoside triphosphate chromatin-associated

Query Match          9.3%   Score 219;  DB 2;  Length 508;
Best Local Similarity 22.3%; Pred.No. 8.3e-10;
Matches 109; Conservative 83; Mismatches 196; Indels 100; Gaps 21;

Qy  9  SLRVAKVAYPLGLGCVGVYIYVAVIKKHRATQAFFSITRAAPCARMGQQAHSPLGTAAD 68
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  26 SKRTKSIIFIVACVTIALGLLPFG-----YSILRSGNRR----- 61

Qy  69 GHEVFGIMDAGSTGTRVHVFOFTPPRETPLT--HETPKAVK--PGLSAYADVVEKS 124
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  62 -VSLHVSIIIDGSSGSTRVHVFGY-KIESKPVDFGEEENYASLKLSPGLSAYADNPEGV 119
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Qy  125 AQGIRELLDVAKODIPDFDKATPLVLKATAGRLLLPGEKAAQKLQKVKEVFKASPLVG 184
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  120 SESVTELVEPAKKRVHKGLKXSDIRLMATAGRLLELPVQEQIILDVTRVLRSSGFDR 179
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Qy  185 DDCVSI MNGTDEGVSAWITINFITGSLKTPGGSSVGMLDGGSGTOIAFLPRVEGTLOAS 244
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  180 DEWASTVISELNFQDLMKV-YMLGLL-----LIMRSVRLEVTFF-----STELV 223

Qy  245 PGYLTAALRMFNRTKLYSYSLGILGMSARLAILGGVSEQPAKD--CKELV-SPCLIS--- 299
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  224 PSFESRTLAVGNVSYNLYSHSFLDFQDRAAQEKLSYLSNAA NSTGEGIVDPDPCPKGY 283
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Qy  300 -----PSFKGEWEHAEVTRYVSG-----QKAASLHE---LCAARVSEV----- 335
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  284 ILETNL-QKDLPGFLADKGKFTATLQAGNFSECRSAFAFMLEQKCKTYKRCSIGSIFT 343
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Qy  336 --LONRVHRTTEEVKHVDVYAFSVYVDLAGVGLIDAEKGGSLVGD--FEIAAKYVCRTL 391
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  344 PNLQGSFLATE-----NFFHTSKFFGLGKEMSEMLAGKFCGEEWSEKLKVKYP----- 394
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Qy  392 ETQOQSPSPSCMDLTY-VSLLLQEEFGFP-RSKVLKILTRKI--DNVETSWALGAI----- 441
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  395 TPKDENLLRYCFSSAVIISMLHDSLGLVALDDDERIKYASKAGEDIPLDNALGAFINTAT 454
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Qy  442 --FHYIDS 447
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  455 ATFDYSDN 462
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

Search completed: November 16, 2004, 17:00:26
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 16:34:13 ; Search time 196 Seconds
(without alignments)
1338.627 Million cell updates/sec

Title: US-09-905-589A-2

Perfect score: 2364

Sequence: 1 MKTISNHGSLRVAKVAYPLG.....ALGAIFHYDLSLNROKSPAS 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2361	99.9	484	1	ENP6_HUMAN	O75354 homo sapien
2	2361	99.9	503	2	Q8N3H3	Q8n3h3 homo sapien
3	2063.5	87.3	455	1	ENP6_RAT	Q9er31 rattus norv
4	1943	82.2	445	2	Q6YHK4	Q6yhk4 cavia porce
5	1229.5	52.0	278	2	Q8CH23	Aa72326 cavia por
6	1021	43.2	427	2	Q6P6S9	Q6pch3 mus musculu
7	1021	43.2	427	2	AAH62044	Q6p6s9 rattus norv
8	1007	42.6	427	1	ENP5_MOUSE	Aah62044 rattus no
9	1007	42.6	427	2	Q8CD29	Q9wuz9 mus musculu
10	1007	42.6	427	2	Q8CD29	Q8cd29 mus musculu
11	1007	42.6	427	2	AAK82949	Aak82949 mus muscu
12	1007	42.6	427	2	BAC229515	Bac29515 mus muscu
13	1007	42.6	427	2	BAC229861	Bac29861 mus muscu
14	1007	42.6	427	2	BAC37592	Bac37592 mus muscu
15	1007	42.6	427	2	BAC37862	Bac37862 mus muscu
16	1007	42.6	427	2	BAC38219	Bac38219 mus muscu
17	1007	42.6	427	2	BAC40362	Bac40362 mus muscu
18	1000	42.3	427	2	Q8BR23	Q8br23 mus musculu
19	999	42.3	428	1	ENP5_HUMAN	O75356 homo sapien
20	992	42.0	428	2	Q96RX0	Q96rx0 homo sapien
21	959	40.6	469	1	ENP5_MESAU	Q9qyc8 mesocricetu
22	957	40.5	224	2	Q8CD16	Q8cd16 mus musculu
23	636.5	26.9	533	2	Q7PV18	Q7pv18 anopheles g
24	621	26.3	461	2	O76268	O76268 drosophila
25	621	26.3	464	2	Q9VQ18	Q9vq18 drosophila
26	590.5	25.0	479	2	Q9XU84	Q9xu84 caenorhabdi
27	532.5	22.5	595	2	Q6BU56	Q6bu56 debaryomyce
28	531.5	22.5	522	1	GDAL_KLUJIA	Q8hem6 kluyveromyc
29	528	22.3	489	2	Q8HT16	Q8ht16 oryza sativ
30	525.5	22.2	467	2	Q9SPM7	Q9spm7 dolichos bi
31	509	21.5	455	2	Q84UE0	Q84ue0 medicago tr

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32 508 21.5 556 1 GDAL SCHPO
33 506 21.4 462 2 Q9XFC9
34 505.5 21.4 467 2 Q84UD8
35 504.5 21.3 467 2 Q8RV76
36 501.5 21.2 447 2 Q9FUI1
37 501 21.2 455 2 Q9SPM6
38 500 21.2 539 2 Q6CBK6
39 498.5 21.1 541 2 Q6FLR7
40 498 21.1 518 1 GDAL YEAST
41 495 20.9 467 2 Q6Z4P2
42 495 20.9 467 2 BAC83798
43 490 20.7 510 2 Q753F2
44 490 20.7 510 2 Q853733
45 489.5 20.7 471 2 Q9SQG2

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ALIGNMENTS

RESULT 1

ENP6_HUMAN

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ID ENP6_HUMAN STANDARD; PRT: 484 AA.
AC O75354; Q7Z5B5; Q8TAS7; Q9UJD1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
DE (NTPDase6) (CD39 antigen-like 2).
GN Name=ENTPD6; Synonyms=CD39L2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
[1]
SEQUENCE FROM N.A., AND VARIANT VAL-138.
RP TISSUE=Keratinocytes;
RC MEDLINE=98341119; PubMed=9676430;
RA Chadwick B.P., Frischauf A.-M.;
RT "The CD39-like gene family: identification of three new human members
RT (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
RT the gene family from Drosophila melanogaster.";
RL Genomics 50:357-367(1998).
[2]
SEQUENCE FROM N.A.
RP MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RX Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguely C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Clegg S., Copley V.B., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Beck S.,
RA Wilmong L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
[3]

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SEQUENCE FROM N.A., AND SOLUBLE FORM DISULFIDE BONDS.
 PubMed=14529283; DOI=10.1021/bi035137k; Kirley T.L.;
 Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;
 "Bacterial expression, characterization, and disulfide bond
 determination of soluble human NTPase6 (CD39L2) nucleotidase:
 implications for structure and function.";
 RL Biochemistry 42:11726-11735 (2003).
 [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [5]
 RN SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RP PubMed=11041856; DOI=10.1021/bi009592;
 RA Yeung G., Mulero J.J., McGowan D.W., Bajwa S.S., Ford J.E.;
 RT "CD39L2, a gene encoding a human nucleoside diphosphatase,
 predominantly expressed in the heart.";
 RL Biochemistry 39:12916-12923 (2000).
 CC -!- FUNCTION: Might support glycosylation reactions in the Golgi
 apparatus and, when released from cells, might catalyze the
 hydrolysis of extracellular nucleosides. Hydrolyzes preferentially
 nucleoside 5'-diphosphates, nucleoside 5'-triphosphates are
 hydrolyzed only to a minor extent, there is no hydrolysis of
 nucleoside 5'-monophosphates. The order of activity with different
 substrates is GDP > IDP > UDP = CDP >> ADP (By similarity).
 CC -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
 nucleotide + phosphate.
 CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi. But also
 occurs in a soluble extracellular form.
 CC -!- TISSUE SPECIFICITY: Expressed in most tissues, but predominantly
 in heart.
 CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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 CC
 DR EMBL; AF039916; AAC39883.1; -;
 DR EMBL; AL035252; CAB41571.1; -;
 DR EMBL; AY327581; AAP92131.1; -;
 DR EMBL; BC025980; AAH25980.1; -;
 DR Genbank; HGNC:3368; ENTDP6.
 DR MIM; 603160; -;
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF01150; GDA1_CD39_1;
 DR PROSITE; PS01238; GDA1_CD39_NTPase; FALSE NEG.
 DR KEGG; Glycoprotein; Golgi stack; Hydrolase; Magnesium;
 KW Polymorphism; Signal-anchor; Transmembrane.
 DR

FT DOMAIN 1 39 Cytoplasmic (Potential).
 FT TRANSMEM 40 60 Signal-anchor for type II membrane
 FT protein (Potential).
 FT Lumenal (Potential).
 FT DISULFID 484 In soluble form.
 FT DISULFID 325 In soluble form.
 FT DISULFID 416 In soluble form.
 FT CARBOHYD 220 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 284 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 284 L -> V (in dSNP:1044567).
 FT VARIANT 138 /FTid=VAR.017863.
 FT CONFLICT 14 S -> N (in Ref. 3).
 FT CONFLICT 19 Missing (in Ref. 4).
 FT CONFLICT 202 E -> K (in Ref. 2).
 SQ SEQUENCE 484 AA; 53247 MW; 604C958953179089 CRC64;
 Query Match 99.9%; Score 2361; DB 1; Length 484;
 Best Local Similarity 99.8%; Pred. No. 1.6e-177; Indels 0; Gaps 0;
 Matches 455; Conservative 1; Mismatches 0;
 QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRAATATQAFPSITRAAPGARWGOAH 60
 DB 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRAATATQAFPSITRAAPGARWGOAH 88
 QY 61 SPLGTAADGHEVFYGVIMFDAGSTGTRVHVQFTRPRETPTLTHTFKAVKPGLSAYADD 120
 DB 89 SPLGTAADGHEVFYGVIMFDAGSTGTRVHVQFTRPRETPTLTHTFKAVKPGLSAYADD 148
 QY 121 VEKSAQGIREDLLVAKQDIPDFFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
 DB 149 VEKSAQGIREDLLVAKQDIPDFFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208
 QY 181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMGLDGGSGTQAFPRVEGT 240
 DB 209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMGLDGGSGTQAFPRVEGT 268
 QY 241 LQASPPGYLTALRMFNRTYKLYSYGLGLGMSARLAILGGVEGQAPKDGKELVSPCLSP 300
 DB 269 LQASPPGYLTALRMFNRTYKLYSYGLGLGMSARLAILGGVEGQAPKDGKELVSPCLSP 328
 QY 301 SFKGEWEHAEVTVRVSGQAAASLHELCAARVSEVLQNRVHRTVEVKHVDYAFSYVDL 360
 DB 329 SFKGEWEHAEVTVRVSGQAAASLHELCAARVSEVLQNRVHRTVEVKHVDYAFSYVDL 388
 QY 361 AAGVGLIDAEKGGSLVGVDFEIAKYVCTLETQSPSPSCMDLTYYVSLLLQEGFPERS 420
 DB 389 AAGVGLIDAEKGGSLVGVDFEIAKYVCTLETQSPSPSCMDLTYYVSLLLQEGFPERS 448
 QY 421 KVLXLRKIDNVETSWALGAFHYIDSLNROKSPAS 456
 DB 449 KVLXLRKIDNVETSWALGAFHYIDSLNROKSPAS 484
 RESULT 2
 Q8N3H3 PRELIMINARY; PRT; 503 AA.
 ID Q8N3H3
 AC Q8N3H3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp761J1915 (Fragment).
 GN Name=DKFZp761J1915;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Amysdala;
 RA Ansonge W., Wirkner U., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL834156; CAD38864.1; -;
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR

```

DR Pfam; PF01150; GDA1_CD39; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 503 AA; 54763 MW; 163933PF9139D8DF CRC64;

Query Match 99.9%; Score 2361; DB 2; Length 503;
Best Local Similarity 99.8%; Pred. No. 1.7e-177;
Matches 455; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRKINSHSLRVAKYVPLGLCVGVFIYVYIKWHRATATQAFSITRAAPGARVGOQAH 60
DB |||||
QY 48 MRKINSHSLRVAKYVPLGLCVGVFIYVYIKWHRATATQAFSITRAAPGARVGOQAH 107
DB |||||
QY 61 SPLGTAADGHEVFGIMFDAGSTGRVHVFOFTRPPRETPTLTHTETKAVKPGLSAYADD 120
DB |||||
QY 108 SPLGTAADGHEVFGIMFDAGSTGRVHVFOFTRPPRETPTLTHTETKAVKPGLSAYADD 167
DB |||||
QY 121 VEKSAQGIKRELLDVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP 180
DB |||||
QY 168 VEKSAQGIKRELLDVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP 227
DB |||||
QY 181 FLVGDDCVSINMGTDGVSAMITINFLTGSLSKTPGSSVGMDLGGSGTQTAFLPRVEGT 240
DB |||||
QY 228 FLVGDDCVSINMGTDGVSAMITINFLTGSLSKTPGSSVGMDLGGSGTQTAFLPRVEGT 287
DB |||||
QY 241 LQASPPGYLTALRMFNRYKLYSYLGLGLMSARLAILGGVGGOPAKDGKELVSPCLSP 300
DB |||||
QY 288 LQASPPGYLTALRMFNRYKLYSYLGLGLMSARLAILGGVGGOPAKDGKELVSPCLSP 347
DB |||||
QY 301 SFKGEWEHAEVTVRYVSGOKAAASLHELCAARVSEVLQNRVHRTVHVDFYAFSYYIDL 360
DB |||||
QY 348 SFKGEWEHAEVTVRYVSGOKAAASLHELCAARVSEVLQNRVHRTVHVDFYAFSYYIDL 407
DB |||||
QY 361 AAGVGLIDAEGKSLVVGDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQEFPPRS 420
DB |||||
QY 408 AAGVGLIDAEGKSLVVGDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQEFPPRS 467
DB |||||
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
DB |||||
QY 468 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 503
DB |||||

RESULT 3
ENP6 RAT STANDARD; PRT; 455 AA.
AC Q9ER31;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
DE (NTPDase6) (CD39 antigen-like 2).
GN Name=Entpd6; Synonyms=Cd3912;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.; SUBCELLULAR LOCATION, AND CHARACTERIZATION.
STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=20498744; PubMed=11042116;
RA Braun N.; Fengler S.; Ebeling C.; Servos J.; Zimmermann H.;
RT "Sequencing, functional expression and characterization of rat
RT NTPDase6, a nucleoside diphosphatase and novel member of the ecto-
RT nucleoside triphosphate diphosphohydrolase family.";
RL Biochem. J. 351:639-647(2000)
CC
CC -!- FUNCTION: Might support glycosylation reactions in the Golgi
CC apparatus and, when released from cells, might catalyze the
CC hydrolysis of extracellular nucleotides. Hydrolyzes preferentially
CC nucleoside 5'-diphosphates, nucleoside 5'-triphosphates are
CC hydrolyzed only to a minor extent, there is no hydrolysis of
CC nucleoside 5'-monophosphates. The order of activity with different
CC substrates is GDP > IDP >> UDP = CDP >> ADP.
CC -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a

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CC nucleotide + phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi. But also
CC occurs in a soluble extracellular form.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ277748; CAC16598.1; -.
DR RGD; 619725; Entpd6.
DR InterPro; IPR00407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; FALSE NEG.
KW Calcium; Glycoprotein; Golgi stack; Hydrolase; Magnesium;
KW Signal-anchor; Transmembrane.
FT DOMAIN 1 12
FT TRANSMEM 13 32
FT SIGNAL 33 455
FT DOMAIN 33 455
FT DISULFID 297 327
FT DISULFID 387 401
FT CARBOHYD 192 192
FT CARBOHYD 256 256
FT SEQUENCE 455 AA; 49899 MW; 19A22E8BAEF0F77B CRC64;
SQ
Query Match 87.3%; Score 2063.5; DB 1; Length 455;
Best Local Similarity 86.6%; Pred. No. 4.3e-154;
Matches 394; Conservative 27; Mismatches 33; Indels 1; Gaps 1;
QY 1 MRKINSHSLRVAKYVPLGLCVGVFIYVYIKWHRATATQAFSITRAAPGARVGOQAH 60
DB |||||
QY 1 MRKINSHSLRVAKYVPLGLCVGVFIYVYIKWHRATATQAFSITRAAPGARVGOQAH 60
DB |||||
QY 61 SPLGTAADGHEVFGIMFDAGSTGRVHVFOFTRPPRETPTLTHTETKAVKPGLSAYADD 120
DB |||||
QY 61 SPLGTAADGHEVFGIMFDAGSTGRVHVFOFTRPPRETPTLTHTETKAVKPGLSAYADD 120
DB |||||
QY 121 VEKSAQGIKRELLDVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP 180
DB |||||
QY 121 VEKSAQGIKRELLDVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP 180
DB |||||
QY 181 FLVGDDCVSINMGTDGVSAMITINFLTGSLSKTPGSSVGMDLGGSGTQTAFLPRVEGT 240
DB |||||
QY 181 FLVGDDCVSINMGTDGVSAMITINFLTGSLSKTPGSSVGMDLGGSGTQTAFLPRVEGT 240
DB |||||
QY 241 LQASPPGYLTALRMFNRYKLYSYLGLGLMSARLAILGGVGGOPAKDGKELVSPCLSP 300
DB |||||
QY 241 LQASPPGYLTALRMFNRYKLYSYLGLGLMSARLAILGGVGGOPAKDGKELVSPCLSP 300
DB |||||
QY 301 SFKGEWEHAEVTVRYVSGOKAAASLHELCAARVSEVLQNRVHRTVHVDFYAFSYYIDL 360
DB |||||
QY 301 SFKGEWEHAEVTVRYVSGOKAAASLHELCAARVSEVLQNRVHRTVHVDFYAFSYYIDL 360
DB |||||
QY 361 AAGVGLIDAEGKSLVVGDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQEFPPRS 420
DB |||||
QY 361 AAGVGLIDAEGKSLVVGDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQEFPPRS 420
DB |||||
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPA 455
DB |||||
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPA 455
DB |||||
QY 420 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPA 454
DB |||||
QY 420 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPA 454
DB |||||
RESULT 4
Q6YHK4 PRELIMINARY; PRT; 445 AA.
AC Q6YHK4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mihaylova-Todorova S.T., Choe S.M., Miller L.J., Horowitz B.,
RL Westfall D.P.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY149906; AAN72326.1; -.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF011150; GDAI_CD39; 1.
KW Hydrolase.
SQ SEQUENCE 445 AA; 48357 MW; 890CEFD068405698 CRC64;

Query Match      82.2%; Score 1943; DB 2; Length 445;
Best Local Similarity 82.9%; Pred. No. 1.4e-144;
Matches 377; Conservative 31; Mismatches 37; Indels 10; Gaps 3;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGYFYIYVAYIKWHRATATQAFPSITRAAPGARWGOAH 60
DB 1 MRKIPSHGSLRMTRVAYVLLGLCVGLFYIYVAYIKWQASAPQVLSSI-----AH 51

QY 61 SPLGTAADGHEVFGYIMFDAGSTGTRVHVFOFTPRPTPTLTHTETKAVKPGLSAYADD 120
DB 52 IPVGSAAHALEVFYGYIMFDAGSTGTRVHVFOFARPPGETPTLTHTETKALKPGLSAYADD 111

QY 121 VEKSAQIGIRELLDVAKODIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
DB 112 VEKSAQIGIRELLDVAKODIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 171

QY 181 FLVGDDCVSINMGTDGVSAMITINFLTGSLKTPGGSSVGMMLDLGGGSGTQITFLPRAKGT 240
DB 172 FLVGDDCVSINMGTDGVSAMITINFLTGSLRPRSSVGMMLDLGGGSGTQITFLPRAKGT 231

QY 241 LQASPPGYLTALRMFNRTYKLYSYGLGLMSARLAILGGVEGPAKDGKELVSPCLSP 300
DB 232 LEASPPGHLTSLQMFNRTYKLYSHYGLGLMSARLAILGGVEGPAKDGKELVSPCLSP 291

QY 301 SFKGEWEHAEVTVRVSGQKAAASHHELCAARVSEVLQNRVHRTVEKHVDVFAFSYYIDL 360
DB 292 GFRGEWEHAGITYRISGPK-AGRLHEPCASRVSEVLQSKVHRAEAGHVDVFAFSYYIDL 350

QY 361 AAGVGLIDAEKGGSLVGVDFEIAAKYVCTLTETPOQSPFSCMDLTYVSLLLQEGFPPRS 420
DB 351 AASVGLIDAEKGGSVSLDEFEIAAKYVCTLTGAQPHHSPFLCMLDITYVSLLLREFGFPD 410

QY 421 KVLKLTAKIDNVETSWALGAIFHYIDSLNROKSPA 455
DB 411 KVLKLTAKIDNVETSWALGAIFHYIDSLNROKSPA 445

RESULT 6
Q8CHZ3 PRELIMINARY; PRT; 278 AA.
AC Q8CHZ3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6.
GN Name=Entpd6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038126; AAH38126.1; -.
MGD; MGI:1202295; Entpd6.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
KW Hydrolase.
SQ SEQUENCE 278 AA; 30130 MW; 75A92DD1AC76297F CRC64;

Query Match 52.0%; Score 1229.5; DB 2; Length 278;
Best Local Similarity 85.6%; Pred. No. 1.4e-88;
Matches 237; Conservative 17; Mismatches 18; Indels 5; Gaps 1;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFISITRAAPGARWQQAQ 60
DB 1 MRKIPNHGTLRMWKVAYPLGLCVGLFIYVAYIKWHRASAAQAFITIAAGSARWTQQA 60
QY 61 SPLGTADGHEVYIGIMFDAGSTGRVHVQFTTRPPRETPTLTHTETKAVKPLGSAYADD 120
DB 61 SSPGSAARGHEVYIGIMFDAGSTGRVHVQFARPPGETPTLTHTETKALKPLGSAYADD 120
QY 121 VEKSAQGTRELLDVAKODIPDFWKATPLVLKATAGLLPGLPEKAKQLLKQKVEVFKASP 180
DB 121 VEKSAQGTRELLDVAKODIPDFWKATPLVLKATAGLLPGLPEKAKQLLKQKVEVFKASP 180
QY 181 FLVGGDCVSIINMGTDGVSAMITINFLTGLSKTPGSSVGMGLDGGSGTQTAFILPRVSGT 240
DB 181 FLVGGDCVSIINMGTDGVSAMITINFLTGLSKTPGSSVGMGLDGGSGTQTAFILPRVSGT 240
QY 241 LQASPPGYLTALRMFNRTRYKLYSYSLGLGLMSAPLA 277
DB 241 LQASPPGYLTALRMFNRTRYKLYSYSLGLGLMSAPLA 277
QY 241 LQASPPGYLTALRMFNRTRYKLYSYSLGLGLMSAPLA 277
DB 241 LQASPPGYLTALRMFNRTRYKLYSYSLGLGLMSAPLA 277

RESULT 7
Q6P6S9 PRELIMINARY; PRT; 427 AA.
AC Q6P6S9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5.
GN Name=Entpd5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062044; AAH62044.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
KW Hydrolase.
SQ SEQUENCE 427 AA; 47372 MW; 6CBB44D96A60211 CRC64;

Query Match 43.2%; Score 1021; DB 2; Length 427;
Best Local Similarity 53.2%; Pred. No. 6.9e-72;
Matches 207; Conservative 58; Mismatches 118; Indels 6; Gaps 4;

QY 62 PLGTADGHEVYIGIMFDAGSTGRVHVQFTTRPPRETPTLTHTETKAVKPLGSAYADD 120
DB 39 PNVNSAG---TFYIGIMFDAGSTGRVHVQFTTRPPRETPTLTHTETKAVKPLGSAYADD 95
QY 121 VEKSAQGTRELLDVAKODIPDFWKATPLVLKATAGLLPGLPEKAKQLLKQKVEVFKASP 180
DB 96 PQGAETVQELLEVAKOSIPRSHMKRTPEVLKATAGLLPGLPEKAKQLLKQKVEVFKASP 155
QY 181 FLVGGDCVSIINMGTDGVSAMITINFLTGLSKTPGSSVGMGLDGGSGTQTAFILPRVSGT 240
DB 156 FLVGGDCVSIINMGTDGVSAMITINFLTGLSKTPGSSVGMGLDGGSGTQTAFILPRVSGT 215
QY 241 LQASPPGYLTALRMFNRTRYKLYSYSLGLGLMSAPLA 300
DB 216 LEQTPKGYLASFEMFNSTFKLYTHSYLGFGLKARLATIGALEAE-GTDGHTFRSACLPR 274
QY 301 SFKGWEHAEVTVYVSGQKAAASHLCAARVSEVLQNRVHRTVEKXVDYFASYYDL 360
DB 275 WLEAEWTFGGVKYQYGNQEGEMGFECYAEVRVWQKLPQEPFIRGSSFYAFSYYDR 334
QY 361 AAGVGLIDAEGKGSLLVVGDFEIAAKYVCRTLETQPSPPSCMDLTYYVSLLOE-FGPR 419
DB 335 AAETHLIDYEKGGVLYKVEDFERKAREVCDNLESFSSGSPFLCMDLSYITALLKDGFGFED 394
QY 420 SKVLKTRKIDNVETSWALGAIFHYIDSL 448
DB 395 GTLLQLTKVNNIETGWALGATPHLLQSL 423

RESULT 8
AAH62044 PRELIMINARY; PRT; 427 AA.
AC AAH62044
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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298 GFPCVAEVLVVQKGLHQPEEVRGSAFVAFYVYYDRAADTHLIDYKGGVLKVEDEFRK 357

384 AXVCRTLETQSPGSPFSCMDLTYYVSLLLQEQ-FGPRSKVLKTRKIDNVETSWALGATP 442

358 AREVCNGLSGSSGSPFLCMDLTYYITALLKDGFGPADGTLQLQTKKVNNIETGVALGATP 417

443 HYIDSL 448

418 HLLQSL 423

RESULT 10

Q8CD29

ID Q8CD29 PRELIMINARY; PRT; 427 AA.

AC Q8CD29;

DT 01-MAR-2003 (TRENBLrel. 23, Created)

DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library. Clone:6030456F04 product:ectonucleoside triphosphate diphosphohydrolase 5, full insert sequence.

DE diphosphohydrolase 5, full insert sequence.

GN Name=Entpds;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1] HVIDSL 448

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RC MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RC MEDLINE=21085660; PubMed=11217851;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RA The FANTOM Consortium;

RA "The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RC MEDLINE=20499374; PubMed=11042159;

RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RC MEDLINE=20530913; PubMed=11076861;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP SEQUENCE FROM N.A.


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RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK031581; BAC27461.1; -.
DR MGD: MGI:1321385; Entrepd5.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39; 1.
KW Hydrolase.
SQ
SEQUENCE 427 AA; 47101 MW; 653773C842B58477 CRC64;

Query Match 42.6%; Score 1007; DB 2; Length 427;
Best Local Similarity 50.0%; Pred. No. 8.8e-71;
Matches 213; Conservative 62; Mismatches 133; Indels 18; Gaps 6;

QY 37 ATATQAFSSITRAAPGA-----RWGQ----QAHSPLGTAADGHEVFGIMFDAGSTG 84
DB 2 ATSWGAVFMLIIACVGSITVYRQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58

QY 85 TRVHVFQFT-RPPEPTPLTHETFKAVKPGLSAYADDVEKSAQGIKRELLDVAKODIPDF 143
DB 59 TRIHVYTFVQKTAGQLPFLGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

QY 144 WKATPLVKTAGLRLLPGEKAQKLLQKVKEFKASPFVLVGGDCVSIIMNGTDEGVSAWIT 203
DB 119 WERTPVVLKATAGLRLLPEKQAQALLLEVEEIEFNKSPFLVPDGSVSIIMDSYEGILAWIT 178

QY 204 INFLTGSLKTPGGSSVGMGLDGGSTQIAFLPRVEGTLOASPPGYLTALRMFNRTYKLYS 263
DB 179 VNFLTGQLHGRGQETVGTDLGGASTQITFLPQPEKTELETPRGYLTSEFMFNSTFKLYT 238

QY 264 YSYLGGLGMSARLAILGGVEGQPAKDGKELVSPCLSPFKGEWEHAEVTVYRVSQKAAAS 323
DB 239 HSYLGFLGKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGNQEGEM 297

QY 324 LHELCARVSEVLQNRVHRTVEVKHDFYAFSYYYDLAAGVGLIDAEGKSLVVGDEFEIA 383
DB 298 GFEPCTAEVLRVQKHLQHPVEVGRSFAFYAFYYDRAADTHLIDYEKGGVLYKVEDFERK 357

QY 384 AKYVCRTLETQPSPPSCMDLTVVSLLOE-FGFPRSKVLKTRKIDNVETSWALGAIF 442
DB 358 AREVCDNLGSPSSPFLCMLDTITALLKDGFGFADGTTLLQTLKKNNIETGWALGATF 417

QY 443 HYIDSL 448
DB 418 HLLQSL 423

RESULT 11
ID AAK82949 PRELIMINARY; PRT; 427 AA.
AC AAK82949;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE PcpH proto-oncogene protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=thymus;

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RX MEDLINE=99437879; PubMed=10506756;
RA Recio J.A., Zambiano N., de La Pena L., Powers C., Siwarski D.,
RA Huppi K., Notario V.;
RT "cDNA isolation, expression, and chromosomal localization of the mouse
RT pcpH proto-oncogene.";
RL Mol. Carcinog. 26:130-136(1999).
DR EMBL: AF136571; AAK82949.1; -.
SQ SEQUENCE 427 AA; 47101 MW; 2F9DA2C342C55577 CRC64;

Query Match 42.6%; Score 1007; DB 2; Length 427;
Best Local Similarity 50.0%; Pred. No. 8.8e-71;
Matches 213; Conservative 62; Mismatches 133; Indels 18; Gaps 6;

QY 37 ATATQAFSSITRAAPGA-----RWGQ----QAHSPLGTAADGHEVFGIMFDAGSTG 84
DB 2 ATSWGAVFMLIIACVGSITVYRQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58

QY 85 TRVHVFQFT-RPPEPTPLTHETFKAVKPGLSAYADDVEKSAQGIKRELLDVAKODIPDF 143
DB 59 TRIHVYTFVQKTAGQLPFLGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

QY 144 WKATPLVKTAGLRLLPGEKAQKLLQKVKEFKASPFVLVGGDCVSIIMNGTDEGVSAWIT 203
DB 119 WERTPVVLKATAGLRLLPEKQAQALLLEVEEIEFNKSPFLVPDGSVSIIMDSYEGILAWIT 178

QY 204 INFLTGSLKTPGGSSVGMGLDGGSTQIAFLPRVEGTLOASPPGYLTALRMFNRTYKLYS 263
DB 179 VNFLTGQLHGRGQETVGTDLGGASTQITFLPQPEKTELETPRGYLTSEFMFNSTFKLYT 238

QY 264 YSYLGGLGMSARLAILGGVEGQPAKDGKELVSPCLSPFKGEWEHAEVTVYRVSQKAAAS 323
DB 239 HSYLGFLGKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGNQEGEM 297

QY 324 LHELCARVSEVLQNRVHRTVEVKHDFYAFSYYYDLAAGVGLIDAEGKSLVVGDEFEIA 383
DB 298 GFEPCTAEVLRVQKHLQHPVEVGRSFAFYAFYYDRAADTHLIDYEKGGVLYKVEDFERK 357

QY 384 AKYVCRTLETQPSPPSCMDLTVVSLLOE-FGFPRSKVLKTRKIDNVETSWALGAIF 442
DB 358 AREVCDNLGSPSSPFLCMLDTITALLKDGFGFADGTTLLQTLKKNNIETGWALGATF 417

QY 443 HYIDSL 448
DB 418 HLLQSL 423

RESULT 12
ID BAC29515 PRELIMINARY; PRT; 427 AA.
AC BAC29515;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Adult male bone cDNA, RIKEN full-length enriched library,
DE clone:9830144N04 product:ectonucleoside triphosphate
DE diphosphohydrolase 5, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=21085660; PubMed=11217851;

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[illegible][illegible]

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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Toyata T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK037736; BAC29861.1; -.
KW Hydrolase.
SQ SEQUENCE 427 AA; 47101 MW; 2F9DA2C342C55577 CRC64;
Query Match 42.6%; Score 1007; DB 2; Length 427;
Best Local Similarity 50.0%; Pred. No. 8.8e-71;
Matches 213; Conservative 62; Mismatches 133; Indels 18; Gaps 6;
QY 37 ATATQAFFSITRAAPGA-----RWGQ-----QAHSPLGTAAADGHEVFYGMFDAGSTG 84
Db 2 ATSWGAVFMLIIACVGVSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGMFDAGSTG 58
QY 85 TRHVFOFT-RPPRETPTLTHTFKAVKPGLSAYADVEKSAQGIREFLLDVAKODIPDF 143
Db 59 TRIHYTVFVKTAQQLPFLGEIIFDSVKPLSAFVDQPKQGAETVQSLLEVAKDSIPRSH 118
QY 144 WKATPLVLKATAGURLLPGEAKLQKVEVFASFLPVGDDCVSIMGNDGVSAMIT 203
Db 119 WERTPVVLKATAGURLLPGEAKLQKVEVFASFLPVGDDCVSIMGNDGVSAMIT 178
QY 204 INFLTGSIKTPGSSVGMLDLGGSGSTOAFUPRVGTLQASPPGVLTALRMFNKTYKLYS 263
Db 179 VNFUTGQLHGRQSTVTGLDGGASTQITFLPQEKILEQTPRGYLSFEMFNSTFKLYT 238
QY 264 YSYLGLGIMSARLAILGGVEGQAPKDELVSPCLSPFSFKGEWBAHYTVRVSGQKAAAS 323
Db 239 HSYLGLGILKARLAILGGVEGQAPKDELVSPCLSPFSFKGEWBAHYTVRVSGQKAAAS 297
QY 324 LHELCAARVSEVLQNRVHRTBEVHVDPFYAFSYYYDLAAGVGLIDAEGKSSLVVGDREIA 383
Db 298 GFEPFYAEVLRVQGLHQPEVEVRSAPFYAFSYYYDRAADTHLIDYKGGVLYKVEDFERK 357
QY 384 AKYVCRTLETQPSQSPSCMDLTVVSLLOE-FGPPRSKVLKTRKIDNVETSWALGAIF 442
Db 358 AREVCDNLGSPSSGSPFLCMDLTVITALLKDGFGADFTLLQLYKVNNIETGALGATF 417
QY 443 HYIDSL 448
Db 418 HLLQSL 423
RESULT 14
BAC37592
ID BAC37592 PRELIMINARY; PRT; 427 AA.
AC BAC37592;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DE Adult male urinary bladder cDNA, RIKEN full-length enriched library,
DE clone:9530068a17 product:ectonucleoside triphosphate
DE diphosphohydrolase 5, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
```

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QY 85 TRVHVFOFT-RPPRETPTLTHTFKAVKPGLSAYADDVEKSAQGIREFLLDVAQODIPDF 143
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59 TRIHYVTFVQKTAGQLPFLFEGEIFDSVKPGLSAFVDQPKQAGTVEQLLELVAKDSIPRSH 118
QY 144 WKATPLVLKATAGLRLPGEKAOKLQKVEFKASPLFVGGDCCVSMNGTDEGVSAWIT 203
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 WERTFVVLKATAGLRLPGEKAQALLLEVEEIFKNSPFLVPDGSVIMDGSYEGILAWVT 178
QY 204 INFLTGS�KTPGSSVGMLDLGGGSTQAFIPRVGTTLOASPGLYLTALRMFNRTYKLYS 263
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 VNFLTGQLHGRGQETVGTLDLGGASTQTITFLPQEKTELTQTPRGYLTSPFENFTPKLYT 238
QY 264 YSYLGGLMSARLAILGGVEGQPAKDKELVSPCLSPSKFGEWEHAETVYRVSGQKAAAS 323
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAWIFGGVKYQYGGNQEGEM 297
QY 324 LHELCAARVSEVLQNRVHRTVEVKHVDYAFSYYYDLAGVGLIDAEKGGSLVVGDFEIA 383
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
298 GFEPFCYAEVLRVVQGLKHPQBEVRSAGAFYAFSYYYDRAADTHLIDYKGGVLKVEDFERK 357
QY 384 AKYVCRTELETQPSPPFCMDLTVVSVLLQOE-FGPPRSKVLKTRKIDNVETSWALGAIF 442
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
358 AREVCNLDNGSSFGSPFLCMLTYITALLKDGFGFADGTLQLTKVNNIETGWALGATF 417
QY 443 HYIDSL 448
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
418 HLLQSL 423

```

RESULT 15

```

BAC37862 ID BAC37862 PRELIMINARY; PRT; 427 AA.
AC BAC37862;
AT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DE 3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE clone:A630007L13 product:ectonucleoside triphosphate
DE diphosphohydrolase 5, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to

```

prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).

[5]

SEQUENCE FROM N.A.

```

RT STRAIN=C57BL/6J; TISSUE=Thymus;
RC MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishise T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]

```

SEQUENCE FROM N.A.

```

RT STRAIN=C57BL/6J; TISSUE=Thymus;
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirao T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohse N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK080265; BAC37862.1; -.
KW Hydrolase.
SQ SEQUENCE 427 AA; 47101 MW; 2F9DA2C342C55577 CRC64;

```

Query Match

Best Local Similarity 42.6%; Score 1007; DB 2; Length 427;

Matches 213; Conservative 62; Mismatches 133; Indels 18; Gaps 6;

```

QY 37 ATATCAFFSITRAAPGA-----RMGQ-----QAHSPLGTAAADGHEVFYIMFDAGSTG 84
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 ATSGAVFMLIIACVGSTVFYREQQTFEGVFLSSMCPINVSAG---TFYIMFDAGSTG 58
QY 85 TRVHVFOFT-RPPRETPTLTHTFKAVKPGLSAYADDVEKSAQGIREFLLDVAQODIPDF 143
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59 TRIHYVTFVQKTAGQLPFLFEGEIFDSVKPGLSAFVDQPKQAGTVEQLLELVAKDSIPRSH 118
QY 144 WKATPLVLKATAGLRLPGEKAOKLQKVEFKASPLFVGGDCCVSMNGTDEGVSAWIT 203
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 WERTFVVLKATAGLRLPGEKAQALLLEVEEIFKNSPFLVPDGSVIMDGSYEGILAWVT 178
QY 204 INFLTGS�KTPGSSVGMLDLGGGSTQAFIPRVGTTLOASPGLYLTALRMFNRTYKLYS 263
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 VNFLTGQLHGRGQETVGTLDLGGASTQTITFLPQEKTELTQTPRGYLTSPFENFTPKLYT 238
QY 264 YSYLGGLMSARLAILGGVEGQPAKDKELVSPCLSPSKFGEWEHAETVYRVSGQKAAAS 323
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAWIFGGVKYQYGGNQEGEM 297
QY 324 LHELCAARVSEVLQNRVHRTVEVKHVDYAFSYYYDLAGVGLIDAEKGGSLVVGDFEIA 383
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
298 GFEPFCYAEVLRVVQGLKHPQBEVRSAGAFYAFSYYYDRAADTHLIDYKGGVLKVEDFERK 357
QY 384 AKYVCRTELETQPSPPFCMDLTVVSVLLQOE-FGPPRSKVLKTRKIDNVETSWALGAIF 442
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
358 AREVCNLDNGSSFGSPFLCMLTYITALLKDGFGFADGTLQLTKVNNIETGWALGATF 417
QY 443 HYIDSL 448
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
418 HLLQSL 423

```

Search completed: November 16, 2004, 16:59:41

us-09-905-589a-2.rup

Tue Nov 16 17:15:08 2004

Job time : 201 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 16:32:53 ; Search time 156 Seconds
(without alignments)
1048.593 Million cell updates/sec

Title: US-09-905-589A-2

Perfect score: 2364

Sequence: 1 MRKISNGSLRVAKVAYPLG.....ALGAIFHYDLSLRQKSPAS 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_238Sep04:.*
1: Geneseqpl980s:.*
2: Geneseqpl990s:.*
3: Geneseqpl2000s:.*
4: Geneseqpl2001s:.*
5: Geneseqpl2002s:.*
6: Geneseqpl2003as:.*
7: Geneseqpl2003bs:.*
8: Geneseqpl2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2364	100.0	456	5	AAE19881
2	2364	100.0	456	8	ADQ99442
3	2364	100.0	484	4	AAE19881
4	2364	100.0	484	8	ADQ99442
5	2361	99.9	463	5	ABBO6124
6	2351	99.9	467	5	ABJ04657
7	2351	99.5	456	4	AAW93929
8	2351	99.5	456	8	ADL32067
9	2152	91.0	450	7	ADCL14220
10	2135	90.3	462	4	AAU30882
11	2116	89.5	446	5	ABJ04658
12	2003	84.7	471	4	AAE19881
13	999	42.3	428	3	AAE19881
14	999	42.3	428	4	AAE19881
15	999	42.3	428	4	AAE19881
16	999	42.3	428	5	AAE19881
17	999	42.3	428	8	ADP07487
18	999	42.3	428	8	ADP07487
19	999	42.3	428	8	ADQ99446
20	999	42.3	428	8	ADQ99446
21	996	42.1	428	3	AAV44850
22	996	42.1	428	4	AAE19881
23	992	42.0	428	7	ADJ70490
24	992	42.0	428	8	ADP07489
25	909	38.5	405	3	AAV44851

26	909	38.5	405	4	AAE19881
27	909	38.5	407	8	ADP07491
28	904	38.2	465	5	AAE19881
29	904	38.2	465	8	ADQ99448
30	823	34.8	330	3	AAE19881
31	621	26.3	461	4	ABE66213
32	621	26.3	461	8	ADQ99472
33	621	26.3	464	4	ABE66213
34	596	25.2	141	4	AAU30881
35	596	25.2	144	4	AAU30881
36	518.5	21.9	467	2	AAW85687
37	506	21.4	462	5	AAU78818
38	506	21.4	462	5	AAU78818
39	501	21.2	486	2	AAW85685
40	501	21.2	486	5	AAU78819
41	495	20.9	139	5	ADK36500
42	490	20.7	455	8	ADO60417
43	488.5	20.7	472	6	ABP81286
44	486	20.6	457	7	ABM74049
45	485	20.5	454	7	ADJ57264

ALIGNMENTS

RESULT 1

AAE19881
ID AAE19881 standard; protein; 456 AA.

XX AC AAE19881;

DT 18-JUN-2002 (first entry)

XX Human CD39L2 protein.

DE Human, CD-39-like protein; CD39L2 protein; therapy; immune deficiency;
KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
KW Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;
KW dermatological; immunosuppressive; vulnerable; anticonvulsant;
KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic.

XX Homo sapiens.

XX US6350447-B1.

XX 26-FEB-2002.

XX 29-JAN-1999; 99US-00240639.

XX 29-JAN-1999; 99US-00240639.

XX (HYSE-) HYSEQ INC.

XX Chadwick BP, Frischauf A;

XX WPI: 2002-215262/27.

XX N-PSDB; AAD31693.

PT An isolated polypeptide with phosphohydrolase activity, designated CD39L2, useful to identify other proteins with which binding occurs or identify inhibitors and for treatment of, e.g., Alzheimer's, multiple sclerosis and osteoporosis.

PS Claim 1; Fig 4; 101pp; English.

XX The present invention relates to novel proteins with phosphohydrolase activity, designated CD-39-like (CD39L) proteins and polynucleotides

CC encoding such proteins. CD39L proteins are useful to treat infectious
CC diseases caused by viral, bacterial, fungal or other infection that may
CC be treatable with CD39L. They are useful in the treatment of various
CC immune deficiencies and disorders, autoimmune disorders such as multiple
CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
CC thyroiditis and insulin dependent diabetes mellitus, allergic reactions
CC and conditions such as asthma and other respiratory problems, periodontal
CC disease, osteoporosis, osteoarthritis and other tooth repair processes.
CC They may have utility in compositions used for bone, cartilage, tendon,
CC ligament and/or nerve tissue growth or regeneration as well as for wound
CC healing and tissue repair and replacement and in the treatment of burns,
CC incisions and ulcers. CD39L proteins may also be useful for proliferation
CC of neural cells and for regeneration of nerve and brain tissue, i.e. for
CC the treatment of central nervous system diseases such as Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
CC disease, peripheral nervous system diseases peripheral nerve injuries,
CC peripheral neuropathy and localised neuropathies. They are also used to
CC treat mechanical and traumatic disorders which involve degeneration,
CC death or trauma to neural cells or nerve tissue. CD39L proteins of the
CC invention are also useful to promote better or faster closure of non-
CC healing wounds, including pressure ulcers, ulcers associated with
CC vascular insufficiency and surgical and traumatic wounds. They also
CC exhibit anti-inflammatory activity and may be used to treat inflammatory
CC conditions including chronic or acute conditions), including ischaemia-
CC reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
CC or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
CC disease. The present sequence is human CD39L2 protein

XX SQ Sequence 456 AA;

Query Match 100.0%; Score 2364; DB 5; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.2e-215;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGQOAH 60
Db 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGQOAH 60

QY 61 SPLGTAADGHEVFGIMFDAGSTGTRVHVFOFTPRPTPLTTHETPKAVKPGLSAYADD 120
Db 61 SPLGTAADGHEVFGIMFDAGSTGTRVHVFOFTPRPTPLTTHETPKAVKPGLSAYADD 120

QY 121 VEKSAQGIREDLDVAKQDIPDFFWKATPLVLKATAGLRLPGKAQKLLQKVEVFKASP 180
Db 121 VEKSAQGIREDLDVAKQDIPDFFWKATPLVLKATAGLRLPGKAQKLLQKVEVFKASP 180

QY 181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
Db 181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

QY 241 LQASPPGYLTALRMFNRTYKLYSYGLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300
Db 241 LQASPPGYLTALRMFNRTYKLYSYGLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300

QY 301 SPKGEWEHAEVTVYRVSGQKAAASHLCAARVSEVLQNRVHRTBEVKHVDVFAFSYYDL 360
Db 301 SPKGEWEHAEVTVYRVSGQKAAASHLCAARVSEVLQNRVHRTBEVKHVDVFAFSYYDL 360

QY 361 AAGVGLIDAEKGGSLVGVDFEIAAKYVORTLETOQSPSPFSCMDLTVVSLLLQBFPPRS 420
Db 361 AAGVGLIDAEKGGSLVGVDFEIAAKYVORTLETOQSPSPFSCMDLTVVSLLLQBFPPRS 420

QY 421 KVLKLTAKIDNVEVTSWALGALFHYIDSLNRKSPAS 456
Db 421 KVLKLTAKIDNVEVTSWALGALFHYIDSLNRKSPAS 456

RESULT 2
ADQ99442
ID ADQ99442 standard; protein; 456 AA.
XX AC
XX ADQ99442;

DT 23-SEP-2004 (first entry)
XX Human CD39-like protein, CD39L2.
DE
XX CD39-like protein; gene mapping; molecular weight marker;
KW food supplement; anti-thrombotic; anti-tissue graft rejection agent;
KW ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
KW NTPase; human; enzyme.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
DE Region 100..121
FT /note= "Apyrase region (ACR) I"
FT Region 175..190
FT /note= "Apyrase region (ACR) II"
FT Region 219..239
FT /note= "Apyrase region (ACR) III"
FT Region 245..266
FT /note= "Apyrase region (ACR) IV"
XX
XX US6759214-B1.
XX
XX 06-JUL-2004.
XX
XX 13-JUL-2001; 2001US-00908510.
XX
XX 29-JAN-1999; 99US-00240639.
XX
XX (NUVE-) NUVELO INC.
XX
XX Chadwick BP, Frischauf A;
XX
XX WPI; 2004-515395/49.
XX N-PSDB; ADQ99441.
XX
XX New CD-39-like polypeptides and polynucleotides, useful in chromosome and
XX gene mapping, as molecular weight markers, as food supplements, or as
XX anti-thrombotic or anti-tissue graft rejection agents.
XX
XX Claim 2; SEQ ID NO 2; 104pp; English.
XX
XX The invention relates to novel CD39-like polypeptides (CD39-like
XX nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding
XX such polypeptides. CD39-like polynucleotides may be used as hybridisation
XX probes, PCR primers and in chromosome and gene mapping. Polypeptides of
XX the invention may be used as molecular weight markers, as food
XX supplements, in generating an antibody that specifically binds the
XX polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or
XX for regulating ATP neurotransmission in smooth muscle, peripheral ganglia
XX or brain. Sequences of the invention are useful in modulating ecto-ATPase
XX activity and for identifying compounds that modulate ecto-ATPase
XX activity. The present sequence is human CD39-like protein, CD39L2. Note:
XX This sequence is stated to be the same as that shown in Figures 8 and 9,
XX however the sequence is truncated at it's N-terminal. The longer sequence
XX is represented in ADQ99473.
SQ Sequence 456 AA;

Query Match 100.0%; Score 2364; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.2e-215;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGQOAH 60
Db 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGQOAH 60

QY 61 SPLGTAADGHEVFGIMFDAGSTGTRVHVFOFTPRPTPLTTHETPKAVKPGLSAYADD 120
Db 61 SPLGTAADGHEVFGIMFDAGSTGTRVHVFOFTPRPTPLTTHETPKAVKPGLSAYADD 120

QY 121 VEKSAQGIREDLDVAKQDIPDFFWKATPLVLKATAGLRLPGKAQKLLQKVEVFKASP 180
Db 121 VEKSAQGIREDLDVAKQDIPDFFWKATPLVLKATAGLRLPGKAQKLLQKVEVFKASP 180

Db 121 VEKSAQGIREDLVAKQDIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
 Qy 181 FLVGDDCVSINMGTHDEGVSAWITINFLTSGSLKTPGGSSVGMLDLGGSGTQIAFLPRVEGT 240
 Db 181 FLVGDDCVSINMGTHDEGVSAWITINFLTSGSLKTPGGSSVGMLDLGGSGTQIAFLPRVEGT 240
 Qy 241 LQASPPGYLTALRMFNRTYKLYSYSLGGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
 Db 241 LQASPPGYLTALRMFNRTYKLYSYSLGGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
 Qy 301 SFKGEWEHAEVTVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDYFAYSYYDL 360
 Db 301 SFKGEWEHAEVTVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDYFAYSYYDL 360
 Qy 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRITETQPSPPSCMDLTVVSLLLQEGFPFRS 420
 Db 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRITETQPSPPSCMDLTVVSLLLQEGFPFRS 420
 Qy 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
 Db 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456

RESULT 3
 AAB72241
 ID AAB72241 standard; protein; 484 AA.
 XX
 AC AAB72241;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Human CD39 like protein CD39-L2 amino acid sequence.
 XX
 KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
 KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 KW cerebral artery thrombosis; platelet aggregation; inflammation;
 KW apoptosis; autoimmune disorder; neurological disorder;
 KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L2.
 XX
 OS Homo sapiens.
 XX
 PN WO200110205-A1.
 XX
 PD 15-FEB-2001.
 XX
 PF 09-AUG-2000; 2000WO-US021790.
 XX
 PR 09-AUG-1999; 99US-00370265.
 PR 11-JAN-2000; 2000US-00481238.
 PR 25-APR-2000; 2000US-00557800.
 PR 26-MAY-2000; 2000US-00583231.
 PR 30-JUN-2000; 2000US-00608285.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Ford J, Mulero JJ, Yeung G;
 XX
 DR WPI; 2001-147489/15.
 DR N-PSDB; AAF63386.
 XX
 PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
 PT and/or NDPase activity, which are useful in the treatment of pathological
 PT conditions caused by thrombosis (e.g. myocardial infarction) and
 PT inflammatory disorders.
 XX
 PS Claim 39; Page 162-164; 203pp; English.
 XX
 CC This invention relates to polynucleotides encoding human CD39-like
 CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
 CC ATPDase, including NDPase, activity are useful for inhibiting platelet
 CC function and can therefore be used in the prophylaxis or treatment of
 CC pathological conditions caused by or involving thrombosis or excessive
 CC coagulation or excessive platelet aggregation, such as myocardial

CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
 CC artery thrombosis or intracardiac thrombosis, and conditions associated
 CC with venous thrombosis. CD39-L2 and CD39-L2 polypeptides are useful in
 CC modulating disease states (including platelet aggregation, inflammation
 CC and apoptosis) associated with ADP or other purinergic signalling by
 CC reducing the levels of NDPs. The polypeptides are also useful for
 CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or
 CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
 CC cytokine overstimulation); autoimmune disorders such as thrombosis,
 CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
 CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
 CC neurological disorders including neurodegenerative diseases, epilepsy,
 CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, and amyotrophic lateral sclerosis; and cancer. The present
 CC sequence represents human CD39 like protein CD39-L2
 XX
 SQ Sequence 484 AA;
 Query Match 100.0%; Score 2364; DB 4; Length 484;
 Best Local Similarity 100.0%; Pred. NO. 1.3e-215;
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGOAH 60
 Db 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGOAH 88
 Qy 61 SPLGTAADGHEVFYGINFMDAGSTGTRVHVFTQTRPPRETPTLTHTETKAVKPGLSAYADD 120
 Db 89 SPLGTAADGHEVFYGINFMDAGSTGTRVHVFTQTRPPRETPTLTHTETKAVKPGLSAYADD 148
 Qy 121 VEKSAQGIREDLVAKQDIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
 Db 149 VEKSAQGIREDLVAKQDIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208
 Qy 181 FLVGDDCVSINMGTHDEGVSAWITINFLTSGSLKTPGGSSVGMLDLGGSGTQIAFLPRVEGT 240
 Db 209 FLVGDDCVSINMGTHDEGVSAWITINFLTSGSLKTPGGSSVGMLDLGGSGTQIAFLPRVEGT 268
 Qy 241 LQASPPGYLTALRMFNRTYKLYSYSLGGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
 Db 269 LQASPPGYLTALRMFNRTYKLYSYSLGGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328
 Qy 301 SFKGEWEHAEVTVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDYFAYSYYDL 360
 Db 329 SFKGEWEHAEVTVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDYFAYSYYDL 388
 Qy 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRITETQPSPPSCMDLTVVSLLLQEGFPFRS 420
 Db 389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRITETQPSPPSCMDLTVVSLLLQEGFPFRS 448
 Qy 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
 Db 449 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484

RESULT 4
 ADQ99473
 ID ADQ99473 standard; protein; 484 AA.
 XX
 AC ADQ99473;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human CD39-like protein, CD39L2.
 XX
 KW CD39-like protein; gene mapping; molecular weight marker;
 KW food supplement; anti-thrombotic; anti-tissue graft rejection agent;
 KW ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
 KW NDPase; human; enzyme.
 XX
 OS Homo sapiens.
 XX

PN US6759214-B1.
 XX 06-JUL-2004.
 XX 13-JUL-2001; 2001US-00908510.
 XX 29-JAN-1999; 99US-00240639.
 XX (NUVE-) NUVELO INC.
 PA Chadwick BP, Frischauf A;
 PI WPI; 2004-515395/49.
 XX N-PSDB; ADQ99441, ADQ99441.
 DR New CD-39-like polypeptides and polynucleotides, useful in chromosome and
 XX gene mapping, as molecular weight markers, as food supplements, or as
 XX anti-thrombotic or anti-tissue graft rejection agents.
 XX Claim 2; Fig 8A-D; 104pp; English.
 XX The invention relates to novel CD39-like polypeptides (CD39-like
 CC nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding
 CC such polypeptides. CD39-like polynucleotides may be used as hybridisation
 CC probes, PCR primers and in chromosome and gene mapping. Polypeptides of
 CC the invention may be used as molecular weight markers, as food
 CC supplements, in generating an antibody that specifically binds the
 CC polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or
 CC for regulating ATP neurotransmission in smooth muscle, peripheral ganglia
 CC or brain. Sequences of the invention are useful in modulating ecto-ATPase
 CC activity and for identifying compounds that modulate ecto-ATPase
 CC activity. The present sequence is human CD39-like protein, CD39L2. Note:
 CC This sequence is stated to be the same as that shown in SEQ ID 2 of the
 CC sequence listing, however this sequence is longer at the N-terminal. The
 CC shorter sequence is represented in ADQ99442.
 XX
 XX Sequence 484 AA;
 QY Query Match 100.0%; Score 2364; DB 8; Length 484;
 DB Best Local Similarity 100.0%; Pred. No. 1.3e-215;
 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVYIKWHRATATQAFPSITRAAPGARWGQOAH 60
 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVYIKWHRATATQAFPSITRAAPGARWGQOAH 88
 QY 61 SPLGTAADGHEVFYGVIMFDAGSTGTRVHVQFTRPPRETTLTHETPKAVKPGLSAYADD 120
 DB 89 SPLGTAADGHEVFYGVIMFDAGSTGTRVHVQFTRPPRETTLTHETPKAVKPGLSAYADD 148
 QY 121 VEKSAQGIREDLDVAKODIPDFWKATPLVLKATAGLRLLPGEAKQLKQKVEVFKASP 180
 DB 149 VEKSAQGIREDLDVAKODIPDFWKATPLVLKATAGLRLLPGEAKQLKQKVEVFKASP 208
 QY 181 FLVGDDCVSIMNGTDEGVSAWITINFLTSLKTPGGSSVGMGLDGGSGTQIAFLPRVEGT 240
 DB 209 FLVGDDCVSIMNGTDEGVSAWITINFLTSLKTPGGSSVGMGLDGGSGTQIAFLPRVEGT 268
 QY 241 LQASPPGYLTALRNFTNYKLYSYLGLGMSARLAILGGVEQPAKDGKELVSPCLSP 300
 DB 269 LQASPPGYLTALRNFTNYKLYSYLGLGMSARLAILGGVEQPAKDGKELVSPCLSP 328
 QY 301 SFGKEWHAETVYRVSQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDYFAYFSYYDL 360
 DB 329 SFGKEWHAETVYRVSQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDYFAYFSYYDL 388
 QY 361 AAGVGLIDAEKGGSLVGVDFEIAAKYVCRTLETQPSQSPFSCMDLTVYSLLLQBFQPPRS 420
 DB 389 AAGVGLIDAEKGGSLVGVDFEIAAKYVCRTLETQPSQSPFSCMDLTVYSLLLQBFQPPRS 448
 QY 421 KVLKLTAKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
 DB 449 KVLKLTAKIDNVETSWALGAIFHYIDSLNRQKSPAS 484

us-09-905-589a-2.rag

RESULT 5
 ABB06124
 ID ABB06124 standard; protein; 463 AA.
 XX
 AC ABB06124;
 XX
 DT 10-MAY-2002 (first entry)
 XX
 DE Human NS protein sequence SEQ ID NO:216.
 XX
 XX Human; cytostatic; osteopathic; gynaecological; neuroprotective;
 KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
 KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
 KW anorectic; muscular; antinfertility; cardiovascular; anticoagulant;
 KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
 KW anticonvulsant; antidiabetic; tranquiliser; antidepressant; neuroleptic;
 KW gastrointestinal; virucide; antiulcer; antitumor; cerebroprotective; nootropic;
 KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
 KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
 KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
 KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
 KW infertility; cardiovascular disease; coagulation disease; hypertension;
 KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
 KW gastric ulcer; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200206315-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001WO-IL000653.
 XX
 PR 18-JUL-2000; 2000IL-00137345.
 PR 15-DEC-2000; 2000IL-00140354.
 XX
 XX (COMP-) COMPUGEN LTD.
 XX
 PA Mintz L, Freilich S, Bernstein J;
 PI
 XX WPI; 2002-155037/20.
 DR N-PSDB; ABL39778.
 DR
 XX One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
 PT
 XX Claim 6; Page 251-253; 290pp; English.
 PS
 XX ABL39691 to ABL39818 represent novel human nucleic acid sequences
 CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
 CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
 CC antirheumatic, antiarthritic, antipsoriatic, cardiovascular, ophthalmological,
 CC vasotropic, antiarteriosclerotic, antinfertility, cardiovascular, dermatological,
 CC anorectic, muscular, anti-HIV, antinfertility, cardiovascular, cardiant,
 CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant,
 CC immunomodulator, anticonvulsant, antidiabetic, tranquiliser, antitumor,
 CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
 CC nootropic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antitense therapy. Nucleic acids, expression vectors and
 CC antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive
 XX
 XX Sequence 463 AA;

Query Match		99.9%;	Score 2361;	DB 5;	Length 463;
Best Local Similarity		99.8%;	Pred. No. 2.3e-215;		
Matches 455;		Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQAQ	60		
Db	8	MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQAQ	67		
QY	61	SPLGTAADGHEVFGIMFDAGSTGTRVHVQFTRPPRETPTLTHTFKAQKLLQKVEFKASP	120		
Db	68	SPLGTAADGHEVFGIMFDAGSTGTRVHVQFTRPPRETPTLTHTFKAQKLLQKVEFKASP	127		
QY	121	VEKSAQGIREDLVAKQDIPDFFWKATPLVLKATAGLRLPGEKAQKLLQKVEFKASP	180		
Db	128	VEKSAQGIREDLVAKQDIPDFFWKATPLVLKATAGLRLPGEKAQKLLQKVEFKASP	187		
QY	181	FLVGDDCVSIMGTDGVSAMITINFLTGSLKTPGGSSVGMIDLGGGQSTQIAFLPRVEGT	240		
Db	188	FLVGDDCVSIMGTDGVSAMITINFLTGSLKTPGGSSVGMIDLGGGQSTQIAFLPRVEGT	247		
QY	241	LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVGPQAKDGKELVSPCLSP	300		
Db	248	LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVGPQAKDGKELVSPCLSP	307		
QY	301	SFKGEWEHAETVRYSGQKAAASLHELCAARVSEVLQNRVHRTVEKHVDYAFSYYIDL	360		
Db	308	SFKGEWEHAETVRYSGQKAAASLHELCAARVSEVLQNRVHRTVEKHVDYAFSYYIDL	367		
QY	361	AAGVGLIDAEKGSGLVGDFFIAKYVCTLETQPSFFSCMDLTYSVLLQBFGRPS	420		
Db	368	AAGVGLIDAEKGSGLVGDFFIAKYVCTLETQPSFFSCMDLTYSVLLQBFGRPS	427		
QY	421	KVLKTRKIDNVEVSWALCAIFHYIDSLNRQKSPAS	456		
Db	428	KVLKTRKIDNVEVSWALCAIFHYIDSLNRQKSPAS	463		
RESULT 6					
ABJ04657	ID	ABJ04657	standard; protein; 467 AA.		
AC	ABJ04657;				
XX	11-OCT-2002	(first entry)			
DT	Protein of NOVX 15a	SEQ ID No 36.			
DE					
XX	Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaeamic;				
KW	neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;				
KW	tranquiliser; neuroleptic; antidiabetic; antiulcer; antiinflammatory;				
KW	anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes;				
KW	metabolic disorder; obesity; infectious disease; Alzheimer's disease;				
KW	anorexia; neurodegenerative disorder; Parkinson's disorder; obesity;				
KW	immune disorder; haemopoietic disorder; dyslipidaemia; chronic disease;				
KW	metabolic syndrome X; wasting disorder; cancer; neurological disorder;				
KW	epilepsy; stroke; mental disorder; schizophrenia; gastrointestinal disorder;				
KW	vesicular transport; cystic fibrosis; schizophrenia; goiter;				
KW	diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;				
KW	multiple sclerosis; rheumatoid arthritis; transgenic animal;				
gene therapy.					
XX	Unidentified.				
OS					
PN	WO200246409-A2.				
XX					
XX	13-JUN-2002.				
XX					
XX	06-DEC-2001; 2001WO-US046586.				
PF					
XX					
XX	06-DEC-2000; 2000US-0251660P.				
PR					
PR	12-DEC-2000; 2000US-0255029P.				
PR	08-JAN-2001; 2001US-0260326P.				
PR					

24-JAN-2001; 2001US-0263800P.	Guo X, Li L, Patturajan M, Shinkets RA, Casman SJ, Malyankar UM;
20-FEB-2001; 2001US-0269942P.	Tchernev VT, Vernet CAM, Spytek KA, Shency SG, Alsobrook JP;
24-APR-2001; 2001US-0286183P.	Edinger S, Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog FL;
20-AUG-2001; 2001US-0313627P.	Colman SD, Eisen AJ, Liu X, Padigar M, Spaderna SK, Zerhusen BD;
12-SEP-2001; 2001US-0318712P.	WPI; 2002-547774/58.
(CURA-) CURAGEN CORP.	N-PSDB; ABT05470.
Novel isolated polypeptide, designated NOVX, useful for treating or	
preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and	
metabolic, neurodegenerative, immune and hematopoietic disorders.	
Claim 1; Page 140; 42lpp; English.	
The invention relates to an isolated polypeptide, designated NOVX,	
comprising a sequence fully defined in the specification. The isolated	
protein, its encoding polynucleotide or an antibody created from the	
protein is useful in the manufacture of a medicament for treating a	
syndrome associated with a human disease, preferably a NOVX-associated	
disorder, or for treating or preventing a NOVX-associated disorder in a	
subject, preferably human. The isolated protein, its encoding	
polynucleotide or an antibody created from the protein are also useful	
for treating or preventing metabolic disorders, diabetes, obesity,	
infectious disease, anorexia, neurodegenerative disorder, Alzheimer's	
disease, Parkinson's disorder, immune disorders, haematopoietic	
disorders, and various dyslipidaemias, metabolic disturbances associated	
with obesity, the metabolic syndrome X, wasting disorders associated with	
chronic diseases, and cancer. The isolated protein, its encoding	
polynucleotide or an antibody created from the protein are useful for	
treating or preventing neurological disorders such as epilepsy, stroke,	
mental disorders including mood, anxiety, schizophrenic disorders,	
disorders of vesicular transport such as cystic fibrosis, diabetes,	
mellitus, goiter, gastrointestinal disorders including ulcerative	
colitis, other conditions associated with abnormal vesicle trafficking	
including AIDS, allergic reactions, multiple sclerosis and rheumatoid	
arthritis. A cell comprising the vector of the invention is useful for	
producing non-human transgenic animals. The polynucleotide of the	
invention can be used to treat disorders by gene therapy. This sequence	
represents one of the isolated NOVX proteins of the invention	
Sequence 467 AA;	
Query Match 99.9%; Score 2361; DB 5; Length 467;	
Best Local Similarity 99.8%; Pred. No. 2.4e-215;	
Matches 455; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQAQ 60	
Db 12 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQAQ 71	
QY 61 SPLGTAADGHEVFGIMFDAGSTGTRVHVQFTRPPRETPTLTHTFKAQKLLQKVEFKASP 120	
Db 72 SPLGTAADGHEVFGIMFDAGSTGTRVHVQFTRPPRETPTLTHTFKAQKLLQKVEFKASP 131	
QY 121 VEKSAQGIREDLVAKQDIPDFFWKATPLVLKATAGLRLPGEKAQKLLQKVEFKASP 180	
Db 132 VEKSAQGIREDLVAKQDIPDFFWKATPLVLKATAGLRLPGEKAQKLLQKVEFKASP 191	
QY 181 FLVGDDCVSIMGTDGVSAMITINFLTGSLKTPGGSSVGMIDLGGGQSTQIAFLPRVEGT 240	
Db 192 FLVGDDCVSIMGTDGVSAMITINFLTGSLKTPGGSSVGMIDLGGGQSTQIAFLPRVEGT 251	
QY 241 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVGPQAKDGKELVSPCLSP 300	
Db 252 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVGPQAKDGKELVSPCLSP 311	

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QY 301 SPKGEWEHAETVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDVFAFSYYDL 360
DB 312 SPKGEWEHAETVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDVFAFSYYDL 371
QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKVVCRTLETQPOSSPFCMDLTVVSLLLQEFGFP 420
DB 372 AAGVGLIDAEKGGSLVVGDFEIAAKVVCRTLETQPOSSPFCMDLTVVSLLLQEFGFP 431
QY 421 KVLKLRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
DB 432 KVLKLRKIDNVETSWALGAIFHYIDSLNRQKSPAS 467

RESULT 7
AAM93929
ID AAM93929 standard; protein; 456 AA.
XX AC AAM93929;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide, SEQ ID NO: 4100.
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX OS Homo sapiens.
XX PN EP1130094-A2.
XX PD 05-SEP-2001.
XX PF 07-JUL-2000; 2000EP-00114089.
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183765.
XX PA (HELI-) HELIX RES INST.
XX QY Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI: 2001-524255/58.
XX DR N-PSDB; AAK94892.
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX PS Claim 8; SEQ ID NO 4100; 1380pp + Sequence Listing; English.
XX SS The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX Sequence 456 AA;
XX SQ Query Match 99.5%; Score 2351; DB 4; Length 456;
XX Best Local Similarity 99.3%; Pred. No. 2e-214;
XX Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKKINHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSSITRAAPGARWQQA 60
DB 1 MKKINHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSSITRAAPGARWQQA 60

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QY 61 SPLGTAADGHEVYFYGIMFDAGSTGTRVHVQFQTRPPRETPTLTHTFKAVKPGLSAYADD 120
DB 61 SPLGTAADGHEVYFYGIMFDAGSTGTRVHVQFQTRPPRETPTLTHTFKAVKPGLSAYADD 120
QY 121 VKSAQGIARELLDVAQDIPDFWKATPLVLKATAGLRLPGKAKQLLQKVEVKFASP 180
DB 121 VKSAQGIARELLDVAQDIPDFWKATPLVLKATAGLRLPGKAKQLLQKVEVKFASP 180
QY 181 FLVGDDCVSLMNGTDEGVSAWITINFLTGLSKTPGGSSVGMGLDGGGSGTQIAFLPRVEGT 240
DB 181 FLVGDDCVSLMNGTDEGVSAWITINFLTGLSKTPGGSSVGMGLDGGGSGTQIAFLPRVEGT 240
QY 241 LQASPPGYLTALRMFNRTKLYSYSLGGLGMSARLAILGGVGGQPAKQKVEVSPCLSP 300
DB 241 LQASPPGYLTALRMFNRTKLYSYSLGGLGMSARLAILGGVGGQPAKQKVEVSPCLSP 300
QY 301 SPKGEWEHAETVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDVFAFSYYDL 360
DB 301 SPKGEWEHAETVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDVFAFSYYDL 360
QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKVVCRTLETQPOSSPFCMDLTVVSLLLQEFGFP 420
DB 361 AAGVGLIDAEKGGSLVVGDFEIAAKVVCRTLETQPOSSPFCMDLTVVSLLLQEFGFP 420
QY 421 KVLKLRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
DB 421 KVLKLRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456

RESULT 8
ADL32067
ID ADL32067 standard; protein; 456 AA.
XX AC ADL32067;
XX DT 20-MAY-2004 (first entry)
XX DE Human protein encoded by a full length cDNA clone SeqID 4100.
XX KW human; medicine; signal transduction; glycoprotein; transcription;
XX oligo-capping method.
XX OS Homo sapiens.
XX PN EPI396543-A2.
XX PD 10-MAR-2004.
XX PF 07-JUL-2000; 2003EP-00025638.
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183865.
XX PR 07-JUL-2000; 2000EP-00114089.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX QY Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI: 2004-204755/20.
XX DR N-PSDB; ADL32066.
XX PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX length human cDNAs.
XX PS Example 1; SEQ ID NO 4100; 1340pp; English.
XX CC This invention relates to a novel primers useful for synthesising full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes

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CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'
 CC ends using the oligo-capping method. This polypeptide sequence is a full
 CC length human protein of the invention.

XX Sequence 456 AA;

Query Match 99.5%; Score 2351; DB 8; Length 456;
 Best Local Similarity 99.3%; Pred. No. 28-214; 2; Mismatches 0; Gaps 0;
 Matches 453; Conservative 1; Indels 0; Gaps 0;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWGQQA 60
 DB 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWGQQA 60

QY 61 SPLGTAADGHEVFYGVIMFDAGSTGRVHVQFTRPPRETPTLTHTFKAKPGLSAYADD 120
 DB 61 SPLGTAADGHEVFYGVIMFDAGSTGRVHVQFTRPPRETPTLTHTFKAKPGLSAYADD 120

QY 121 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVEFKASP 180
 DB 121 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVEFKASP 180

QY 181 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGSSVGMLDLGGGSTQIAFLPRVEGT 240
 DB 181 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGSSVGMLDLGGGSTQIAFLPRVEGT 240

QY 241 LOASPPGYLTALRPNRYTKLYSYLGLGLMSARLAILGGVEGQPAKGKELVSPCLSP 300
 DB 241 LOASPPGYLTALRPNRYTKLYSYLGLGLMSARLAILGGVEGQPAKGKELVSPCLSP 300

QY 301 SFKEWEHAEVTVYRVSQKAAASHELCAARVSEVLQNRVHRTKRVHDEVFAYSYVDL 360
 DB 301 SFKEWEHAEVTVYRVSQKAAASHELCAARVSEVLQNRVHRTKRVHDEVFAYSYVDL 360

QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLTETQPSQSFSCMDLTYVSLLLQEFGRPS 420
 DB 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLTETQPSQSFSCMDLTYVSLLLQEFGRPS 420

QY 421 KVLKLTTRKIDNVTSWALGAFHYIDSLNRQKSPAS 456
 DB 421 KVLKLTTRKIDNVTSWALGAFHYIDSLNRQKSPAS 456

RESULT 9
 ID ADCL4220 standard; protein; 450 AA.

AC ADCL4220;

DT 18-DEC-2003 (first entry)

XX Human enzyme ENZM-26.

XX enzyme; human; ENZM; cytosolic; antiarteriosclerotic; antidiabetic;
 KW anticonvulsant; neurotropic; neuroprotective; cerebroprotective; anti-HIV;
 KW antiallergic; antiinflammatory; thymometric; gene therapy;
 KW cell proliferative disorder; endocrine disorder; neurological disorder;
 KW immune system disorder; inflammatory disorder; developmental disorder;
 KW reproductive disorder; vesicle-trafficking disorder; infection.

XX Homo sapiens.

PN WO2003042357-A2.

XX 22-MAY-2003.

PF 26-SEP-2002; 2002WO-US031096.

PR 28-SEP-2001; 2001US-0326388P.

PR 12-OCT-2001; 2001US-0328979P.

PR 19-OCT-2001; 2001US-0346034P.

PR 26-OCT-2001; 2001US-0348284P.
 PR 08-NOV-2001; 2001US-0338048P.
 PR 16-NOV-2001; 2001US-0332340P.
 PR 14-DEC-2001; 2001US-0340357P.
 PR 29-MAR-2002; 2002US-0368722P.
 PR 29-MAR-2002; 2002US-0368799P.
 PR 17-MAY-2002; 2002US-0381558P.
 PR 07-JUN-2002; 2002US-0387119P.
 PR 21-JUN-2002; 2002US-0390662P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Yang J, Lu DAM, Yue H, Elliott VS, Warren BA, Duggan BM,
 PI Forsythe LJ, Lee EA, Hafalia AJA, Ramkumar J, Chawla NK, Baughn MR;
 PI Becha SD, Gorvad AE, Tran UK, Li JX, Yao MG, Ison CH, Griffin JA;
 PI Lee SY, Chang H, Emerling BM, Tang YT, Lal PG, Kable AE;
 PI Marquis JP, Jiang X, Jackson AA, Zebajradian Y, Swarnakar A;
 PI Wilson AD, Jin P, Richardson TW, Bhatia U, Burrill JD, Lee S;
 PI Blake JJ, Ho A, Zheng W, Gao J;
 XX WPI; 2003-449567/42.
 DR N-PSDB; ADCL4273.
 XX New human enzymes (ENZM), useful for diagnosing, treating and preventing
 PT diseases or conditions associated with the aberrant ENZM expression e.g.
 PT cancer, diabetes, epilepsy, or infections.
 XX Claim 1; SEQ ID NO 26; 416pp; English.
 XX The invention relates to a novel isolated human enzyme (ENZM)
 CC polypeptide. A polypeptide of the invention has cytostatic,
 CC antiarteriosclerotic, antidiabetic, anticonvulsant, neurotropic,
 CC neuroprotective, cerebroprotective, anti-HIV, antiallergic,
 CC antiinflammatory, and thymometric activity. A polynucleotide encoding a
 CC polypeptide of the invention may have a use in gene therapy. The
 CC polypeptides and polynucleotides are useful in diagnosing, treating and
 CC preventing diseases or conditions associated with the decreased
 CC expression or overexpression of ENZM, such as cell proliferative (e.g.
 CC cancer, atherosclerosis), endocrine (e.g. diabetes), neurological (e.g.
 CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
 CC allergies), developmental (e.g. Hypothyroidism, Cushing's syndrome),
 CC reproductive and vesicle-trafficking disorders, or infections. These are
 CC also useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acid and amino acid sequences of ENZM. The ENZM or
 CC its fragments are useful in screening compounds for effectiveness as
 CC agonist or antagonist of the polypeptides, or in altering the expression
 CC of the target polynucleotide and compounds that specifically bind to or
 CC modulate the activity of the polypeptide. The microarray is useful in
 CC monitoring or measuring protein-protein interactions, drug-target
 CC interactions, and gene expression profiles. The sequences shown in
 CC ADCL4195-ADCL4247 represent ENZM proteins of the invention.

XX Sequence 450 AA;

Query Match 91.0%; Score 2152; DB 7; Length 450;
 Best Local Similarity 92.3%; Pred. No. 1.7e-195;
 Matches 421; Conservative 1; Mismatches 0; Indels 34; Gaps 1;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWGQQA 60
 DB 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWGQQA 88

QY 61 SPLGTAADGHEVFYGVIMFDAGSTGRVHVQFTRPPRETPTLTHTFKAKPGLSAYADD 120
 DB 89 SPLGTAADGHEVFYGVIMFDAGSTGRVHVQFTRPPRETPTLTHTFKAKPGLSAYADD 148

QY 121 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVEFKASP 180
 DB 149 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVEFKASP 208

QY 181 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGSSVGMLDLGGGSTQIAFLPRVEGT 240
 DB 209 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGSSVGMLDLGGGSTQIAFLPRVEGT 268

QY 241 LQASPPGYLTALRMFNRTYKLYSYGLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300
 Db 269 LQASPPGYLTALRMFNRTYKLYSYGLGLGMSARLAILGGVEGQ----- 314
 QY 301 SFKGEWEHAEVTVYRVSGQKAAASLHELCAARVSEVLQNRVHRTTEEVKHVDVFAFSYYDL 360
 Db 315 -----AASLHELCAARVSEVLQNRVHRTTEEVKHVDVFAFSYYDL 354
 QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRILETOPQSSPSCMDLTYVSLLLQEFGEFPRS 420
 Db 355 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRILETOPQSSPSCMDLTYVSLLLQEFGEFPRS 414
 QY 421 KVLKLTTRKIDNVETSWALGAIHFHYIDSLNRQKSPAS 456
 Db 415 KVLKLTTRKIDNVETSWALGAIHFHYIDSLNRQKSPAS 450

RESULT 10
 AAU30882
 ID AAU30882 standard; protein; 462 AA.
 AC AAU30882;
 XX
 DT 18-DEC-2001 (first entry)
 DE Novel human secreted protein #1373.
 XX

Human; vaccination; gene therapy; nutritional supplement;
 stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 KW
 KW
 KW
 KW
 OS Homo sapiens.

XX WO200179449-A2.
 XX 25-OCT-2001.
 XX 16-APR-2001; 2001WO-US008656.
 XX 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-611725/70.
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 XX vaccination, testing and therapy.

XX Claim 20; Page 365; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 XX secreted proteins of the invention

XX Sequence 462 AA;

Query Match 90.3%; Score 2135; DB 4; Length 462;
 Best Local Similarity 92.1%; Pred. No. 7.5e-194;
 Matches 422; Conservative 2; Mismatches 8; Indels 26; Gaps 3;
 QY 1 MRKISNHSGLRVAKVAYPLGLCVGVFIYVYIKWHIRATATQAFSITRAAPGARWGOAH 60
 Db 29 MRKISNHSGLRVAKVAYPLGLCVGVFIYVYIKWHIRANATQAFSITRAAPGARWGOAH 88
 QY 61 SPLGTADAGHEVFVGMEDAGSTGTRVHFQFTRPPRETPLTTHETKAVKPGLSAYADD 120
 Db 89 SPLGTADAGHEVFVGMEDAGSTGTRVHFQF-----YADD 124
 QY 121 VEKSAQGIREDLLVAKODIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVEVFKASP 180
 Db 125 VEKSAQGIREDLLVAKODIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVEVFKASP 194
 QY 181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSIKTPGGSSVGMLDLGGGSTQIVFLTHVEGT 240
 Db 185 FLVGDDCVSIMNGTDEGVSAWITINFLTGSIKTPRRSNVGMLDLGGGSTQIVFLTHVEGT 244
 QY 241 LQASPPGYLTALRMFNRTYKLYSYGLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300
 Db 245 LQASPPGYLTALRMFNRTYKLYSYGLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 304
 QY 301 SFKGEWEHAEVTVYRVSGQKAAASLHELCAARVSEVLQNRVHRTTEEVKHVDVFAFSYYDL 360
 Db 305 SFKGEWEHAEVTVYRVSGQKAAASLHELCAARVSEVLQNRVHRTTEEVKHVDVFAFSYYDL 364
 QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRILETOPQSSPSCMDLTYVSLLLQEFGEF 418
 Db 365 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRILETOPQSSPSCMDLTYVSLLLQEFGEF 424
 QY 419 RSKVLKLTTRKIDNVETSWALGAIHFHYIDSLNRQKSPAS 456
 Db 425 RSKVLKLTTRKIDNVETSWALGAIHFHYIDSLNRQKSPAS 462

RESULT 11
 ABJ04658

ID ABJ04658 standard; protein; 446 AA.

AC ABJ04658;

DT 11-OCT-2002 (first entry)

DE Protein of NOVX 15b SEQ ID No 38.

XX Cytostatic; antidiabetic; anorectic; metabolic; neurotropic; antilipaeamic;
 KW neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;
 KW tranquiliser; neuroleptic; antidiabetic; antitumor; antiinflammatory;
 KW anti-HIV; antiallergic; antirheumatic; antithrombotic; NOX; diabetes;
 KW metabolic disorder; obesity; infectious disease; Alzheimer's disease;
 KW anorexia; neurodegenerative disorder; Parkinson's disorder; obesity;
 KW immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;
 KW metabolic syndrome X; wasting disorder; cancer; neurological disorder;
 KW epilepsy; stroke; mental disorder; schizophrenic disorders; goiter;
 KW vesicular transport; cystic fibrosis; gastrointestinal disorder;
 KW diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
 KW multiple sclerosis; rheumatoid arthritis; transgenic animal;
 KW gene therapy.

OS Unidentified.

XX WO200246409-A2.

PN 13-JUN-2002.

XX 06-DEC-2001; 2001WO-US046586.

XX 06-DEC-2000; 2000US-0251660P.

PR 12-DEC-2000; 2000US-0255029P.

PR 08-JAN-2001; 2001US-0260326P.

PR 24-JAN-2001; 2001US-0263800P.
 PR 20-FEB-2001; 2001US-0269942P.
 PR 24-APR-2001; 2001US-0286183P.
 PR 20-AUG-2001; 2001US-0313627P.
 PR 12-SEP-2001; 2001US-0318712P.
 XX (CURA-) CURAGEN CORP.
 PA Guo X, Li L, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM;
 PI Tchernev VT, Vernet CM, Spytek KA, Shenoy SG, Alsobrook JP;
 PI Edinger S, Feyman JA, Stone DJ, Ellerman K, Gangoli EA, Boldog FI;
 PI Colman SD, Eisen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD;
 XX WPI; 2002-547774/58.
 DR N-PSDB; ABT05471.
 XX Novel isolated polypeptide, designated NOVX, useful for treating or
 PT preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and
 PT metabolic, neurodegenerative, immune and hematopoietic disorders.
 XX Claim 1; Page 141; 421pp; English.
 CC The invention relates to an isolated polypeptide, designated NOVX,
 CC comprising a sequence fully defined in the specification. The isolated
 CC protein, its encoding polynucleotide or an antibody created from the
 CC protein is useful in the manufacture of a medicament for treating a
 CC syndrome associated with a human disease, preferably a NOVX-associated
 CC disorder, or for treating or preventing a NOVX-associated disorder in a
 CC subject, preferably human. The isolated protein, its encoding
 CC polynucleotide or an antibody created from the protein are also useful
 CC for treating or preventing metabolic disorders, diabetes, obesity,
 CC infectious disease, anorexia, neurodegenerative disorder, Alzheimer's
 CC disease, Parkinson's disorder, immune disorders, haematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, the metabolic syndrome X, wasting disorders associated with
 CC chronic diseases, and cancer. The isolated protein, its encoding
 CC polynucleotide or an antibody created from the protein are useful for
 CC treating or preventing neurological disorders such as epilepsy, stroke,
 CC mental disorders including mood, anxiety, schizophrenic disorders,
 CC disorders of vesicular transport such as cystic fibrosis, diabetes
 CC mellitus, goiter, gastrointestinal disorders including ulcerative
 CC colitis, other conditions associated with abnormal vesicle trafficking
 CC including AIDS, allergic reactions, multiple sclerosis and rheumatoid
 CC arthritis. A cell comprising the vector of the invention is useful for
 CC producing non-human transgenic animals. The polynucleotide of the
 CC invention can be used to treat disorders by gene therapy. This sequence
 CC represents one of the isolated NOVX proteins of the invention
 XX SQ Sequence 446 AA;

Query Match 89.5%; Score 2116; DB 5; Length 446;
 Best Local Similarity 91.0%; Pred. No. 4.6e-192;
 Matches 415; Conservative 1; Mismatches 2; Indels 38; Gaps 1;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPCARWGQOAH 60
 DB 29 MRKISNHGSLRVAV-----ARWGQOAH 50

QY 61 SPLGTADGHEVFGIMFDAGSTGRVHVFOFTPPRETPTLTHTFKAVKPGLSAYADD 120
 DB 51 SPLGTADGHEVFGIMFDAGSTGRVHVFOFTPPRETPTLTHTFKALKPGLSAYADD 110

QY 121 VEKSAQGIREDLLDAKQDIPDFWKATPLVLKATAGRLPLGPEKAQKLLQKVGVFKASP 180
 DB 111 VEKSAQGIREDLLDAKQDIPDFWKATPLVLKATAGRLPLGPEKAQKLLQKVGVFKASP 170

QY 181 FLVGDDCVSINMGTDGVSAMITINFLTGLSKTPGSSVGMGLDGGGQSTQIAFLPRVEGT 240
 DB 171 FLVGDDCVSINMGTDGVSAMITINFLTGLSKTPGSSVGMGLDGGGQSTQIAFLPRVEGT 230

QY 241 LQASPPGYLTALRMFNRTYKLYSYSLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
 DB 231 LQASPPGYLTALRMFNRTYKLYSYSLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 290

QY 301 SFGGEWEHAETVYRVSGQKAAASLHELCAARVSEVLQNRVHRTTEVKHVDVFYAFSYVDL 360
 DB 291 SFGGEWEHAETVYRVSGQKAAASLHELCAARVSEVLQNRVHRTTEVKHVDVFYAFSYVDL 350

QY 361 AAGVGLIDAEKGGSLVGDFFIAAKYVCTTETOPQSSPFSCMDLTYYSLLLQEFGPFRS 420
 DB 351 AAGVGLIDAEKGGSLVGDFFIAAKYVCTTETOPQSSPFSCMDLTYYSLLLQEFGPFRS 410

QY 421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 456
 DB 411 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 446

RESULT 12

AAB72242
 ID AAB72242 standard; protein; 471 AA.

XX AC AAB72242;

DT 14-MAY-2001 (first entry)

XX Mature human CD39 like protein CD39-L2 amino acid sequence.

DE Human CD39-like protein; apyrase; NPase; platelet function inhibitor;
 KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 KW cerebral artery thrombosis; platelet aggregation; inflammation;
 KW apoptosis; autoimmune disorder; neurological disorder;
 KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L2.

OS Homo sapiens.

PN WO200110205-A1.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000WO-US021790.

PR 09-AUG-1999; 99US-00370265.

PR 11-JAN-2000; 2000US-00481238.

PR 25-APR-2000; 2000US-00557800.

PR 26-MAY-2000; 2000US-00583231.

PR 30-JUN-2000; 2000US-00608285.

XX (HYSE-) HYSEQ INC.

XX Ford J, Mulero JJ, Yeung G;

XX WPI; 2001-147489/15.

XX N-PSDB; AAF63387.

XX Polynucleotides encoding human CD39-like polypeptides, with apyrase
 PT and/or NPase activity, which are useful in the treatment of pathological
 PT conditions caused by thrombosis (e.g. myocardial infarction) and
 PT inflammatory disorders.

XX Claim 53; Page 192-194; 203pp; English.

XX This invention relates to polynucleotides encoding human CD39-like
 CC polypeptides with apyrase and/or NPase activity. The polypeptides having
 CC ATPase, including NPase, activity are useful for inhibiting platelet
 CC function and can therefore be used in the prophylaxis or treatment of
 CC pathological conditions caused by or involving thrombosis or excessive
 CC coagulation or excessive platelet aggregation, such as myocardial
 CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
 CC artery thrombosis or intracardiac thrombosis, and conditions associated
 CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
 CC modulating disease states (including platelet aggregation, inflammation
 CC and apoptosis) associated with ADP or other purinergic signalling by
 CC reducing the levels of NDPs. The polypeptides are also useful for
 CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or
 CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,

CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis,
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
XX sequence represents mature D39 like protein CD39-L2
SQ Sequence 471 AA;

Query Match 84.7%; Score 2003; DB 4; Length 471;
Best Local Similarity 98.5%; Pred. No. 2.8e-181;
Matches 388; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRKISNHSRLVAKVAVPLGLCVGVFTYVAYIKWHRATATQAFPSITRAAPGARWGQAAH 60
DB 29 MRKISNHSRLVAKVAVPLGLCVGVFTYVAYIKWHRATATQAFPSITRAAPGARWGQAAH 88
QY 61 SPLGTAADGHEVFGIMFDAGSTGRVHVFOFTPPRETPTLTHETPKAVKPGLSAYADD 120
DB 89 SPLGTAADGHEVFGIMFDAGSTGRVHVFOFTPPRETPTLTHETPKAVKPGLSAYADD 148
QY 121 VEKSAQGITRELLDVAKODIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVEKASP 180
DB 149 VEKSAQGITRELLDVAKODIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVEKASP 208
QY 181 FLVGDDCVSIMGNDGVSAMITINFLTGSLKTPGSSVGMGLDLGGGSGTQIAFLPRVEGT 240
DB 209 FLVGDDCVSIMGNDGVSAMITINFLTGSLKTPGSSVGMGLDLGGGSGTQIAFLPRVEGT 268
QY 241 LOASPPGYLTALRMFNRTYKLYSYSLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300
DB 269 LOASPPGYLTALRMFNRTYKLYSYSLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 328
QY 301 SFKGEWEHAEVTVYRVSOGKAAASLHELCAARVSEVLQNRVHRTBEVKHVDVFAFSYYDL 360
DB 329 SFKGEWEHAEVTVYRVSOGKAAASLHELCAARVSEVLQNRVHRTBEVKHVDVFAFSYYDL 388
QY 361 AAGVGLIDAEKGGSLVWGDFFIAAKYVCRTELEQ 394
DB 389 AAGVGLIDAEKGGSLVWGDFFIAAKYGGSHLRE 422

RESULT 13
ID AAY44849
XX AAY44849 standard; protein; 428 AA.
AC AAY44849;
XX
DT 18-MAY-2000 (first entry)
DE Human CD39-L4 protein.
XX
KW CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase;
KW ATP diphosphohydrolase; ATPase; adenosine diphosphate; ADP; treatment;
KW platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
KW cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
KW molecular weight marker; nutritional supplement; tumour; prevention;
KW drug targeting; Apyrase Conserved Region; ACR.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT Protein 23..428
FT /label= Leader_peptide
FT /label= Mature human CD39-L4 protein
FT /note= "Homologous to human and murine CD39"
FT Binding-site 54..58
FT 129..134
FT /label= ATP_Binding_region
FT Region 169..173
FT /label= Apyrase_Conserved_Region
FT Region 169..173

FT /label= Apyrase_Conserved_Region
FT 199..206
FT /note= "Conserved motif in ATPases"
XX
XX WO200004041-A2.
XX 27-JAN-2000.
XX
XX 16-JUL-1999; 99WO-US016180.
XX 16-JUL-1998; 98US-00118205.
XX 24-JUL-1998; 98US-00122449.
XX 04-FEB-1999; 99US-00244444.
XX 19-MAR-1999; 99US-00273447.
XX 09-JUL-1999; 99US-00350836.
XX (HYSE-) HYSEQ INC.
XX Ford J, Mulero J;
XX WPI; 2000-182397/16.
XX N-PSDB; AAZ50356, AAZ50359.
XX New nucleic acid encoding human CD39-like protein, useful for treating
XX and preventing thrombotic disease.
XX Claim 15; Fig 2; 125pp; English.
XX
XX The present amino acid sequence is the CD39-L4 protein, an apyrase and/or
XX nucleotide diphosphatase (NDPase). It is isolated from the human foetal
XX liver-spleen cDNA library, B2HFLS20W. It is a soluble ATP
XX Diphosphohydrolases (ATPase) and is involved in the hydrolysis of
XX adenosine diphosphate (ADP), the agonist that causes platelet
XX aggregation. CD39-L4 protein has 30% and 80% homology to human and murine
XX CD39. It has platelet aggregation inhibition and antithrombotic activity.
XX CD39-L4 is used to treat or prevent thrombosis, myocardial infarction,
XX cerebral ischaemia and angina. It is also used in vitro, to maintain
XX vascular grafts or during extracorporeal circulation, to hydrolyse NDP,
XX as molecular weight markers and as nutritional supplements. It is used to
XX identify therapeutic agents that bind and modulate CD39-L4. It is coupled
XX to toxins for targeting drugs to tumours or other cells that express CD39
XX -L4
XX
SQ Sequence 428 AA;

Query Match 42.3%; Score 999; DB 3; Length 428;
Best Local Similarity 52.4%; Pred. No. 8.6e-86;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

QY 62 PLGTAADGHEVFGIMFDAGSTGRVHVFOFT-PPRETPTLTHETPKAVKPGLSAYADD 120
DB 40 PINVSA---STLYGIMFDAGSTGRVHVFOFT-PPRETPTLTHETPKAVKPGLSAFVDQ 96
QY 121 VEKSAQGITRELLDVAKODIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVEKASP 180
DB 97 PKQGAETVQGLLEVAKOSIPRSHWKKTPVLKATAGLRLLPGEKAQKLLQKVKEVEKASP 156
QY 181 FLVGDDCVSIMGNDGVSAMITINFLTGSLKTPGSSVGMGLDLGGGSGTQIAFLPRVEGT 240
DB 157 FLVPKGSVSIINDGSDGILAWTVNFLTGLHGHRTVGTGLDGGASTQITFLPQPEKT 216
QY 241 LOASPPGYLTALRMFNRTYKLYSYSLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300
DB 217 LEQTPRGYLTSEFMFNSTYKLYSYSLGFGKAAARLATLGALETE-GTDGHTFFSACUPR 275
QY 301 SFKGEWEHAEVTVYRVSOGKAAASLHELCAARVSEVLQNRVHRTBEVKHVDVFAFSYYDL 360
DB 276 WLEAEWIFGGYKYQYGGNQEVEGVEFCYAEVLRVGRKLPQPEVQSGVFAFSYYDR 335
QY 361 AAGVGLIDAEKGGSLVWGDFFIAAKYVCRTELETOPQSSPFCMDLTYVSLLOE-FGPRPR 419
DB 336 AVDTDMIDYKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

PT conditions caused by thrombosis (e.g. myocardial infarction) and
PT inflammatory disorders.

PS Example 9: Page 142-144; 203pp; English; 2014

This invention relates to polynucleotides encoding human CD39-like polypeptides with ADPase and/or NDase activity. The polypeptides having ADPase, including NDase, activity are useful for inhibiting platelet function and can therefore be used in the prophylaxis or treatment of pathological conditions caused by or involving thrombosis or excessive coagulation or excessive platelet aggregation, such as myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral artery thrombosis or intracardiac thrombosis, and conditions associated with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in modulating disease states (including platelet aggregation, inflammation and apoptosis) associated with ADP or other purinergic signalling by reducing the levels of NDPs. The polypeptides are also useful for prophylaxis or treatment of inflammation related disorders, such as disorders involving sepsis or systemic inflammatory response syndrome or SIRS (and associated conditions such as fever, tachycardia, tachypnea, cytokine overstimulation); autoimmune disorders such as thrombosis, atherosclerosis, acute pancreatitis, dermatitis including psoriasis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis; and cancer. The present sequence represents the CD39 like protein CD39-L4 amino acid sequence

Sequence 428 AA;

Query Match 42.3%: Score 999; DB 4: Length 428;

Best Local Similarity 52.4%; Pred. No. 8.6e-86;

Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

QY 62 PLGTAADGHEVFYGYIMFDAGSTGTRVHVVFQFT-RPPRETPTLTHETFFKAVKPGLSAYADD 120

Db 40 PINVSA---STLYGIMFDAGSTGTRIHHVYTFVQKMPGQLPILEGEVFDSPKPLSAFVDQ 96

121 VEKSAOGIRELLDVAKODIPDFWKATPLVLKATAGRLLPGEKAQKLLQKVKEVFKASP 180

Db 97 PKOGAETVOGLLEVAKDSIPRSHWKKTPVVKATAGLRLPEHKAKALLFEVKEIFRKSP 156

181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTOIAFLPRVEGT 240

157 ELVPKGSVSTMDGSDGTLAWVTVNEITGQIHGHROETVGTIDIGGASTOITELPOFEKT 216

241 I Q A S P P G Y I T A I R M F N R T Y K I Y S Y S Y I G I G I M S A R I A I I G G V E G O P A K D G K E I V S P C I S P 300

217 I.EOTPRGVI.TSFEEMFNSTYKI.YTHSVI.GEGI.KAARI.ATI.GALETE-GTDGHTFRSACI.PR 275

301 SEKGEWEHAEVTYRVSGOKAAASI.HEI.CAARVSEVI.ONRVHRTTEEVKHVDEVAESVYYDI. 360

276 WT.EAEWT.EGGVKYVYGGNOEGEVEEPCVAEVT.RVVRGKI.HOPEEVORGSEVAFSVVYDR 335

361 AAGVGLIDAEKGGSLVVGDEETIAAKVVCRTIETPOSSPFCMDITVVSIIIOE-FGEPR 419

336	AVDTDMI	VEKGCIL	KVEDEE	EPKAP	EV	CONI	ENETS	SGSPET	CMND	SVITAI	KDGE	GEAD	395
-----	---------	---------	--------	-------	----	------	-------	--------	------	--------	------	------	-----

420 SKUL KY TRKYDNVETSWAI CATFHYVINDI. 448

396 STVI QI.TKKVNNIETGWAIGATEHTI.I.OSI. 424

Search completed: November 16, 2004, 16:56:11
Job time : 160 secs

Job time : 160 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 16:59:49 ; Search time 142 Seconds
(without alignments)
1136.208 Million cell updates/sec

Title: US-09-905-589A-2

Perfect score: 2364

Sequence: 1 MRKTSNHGSLRVAKVAYPLG.....ALGAIFHYDLSLNKQSPAS 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2364	100.0	484	13	US-10-092-063-27
2	2364	100.0	484	14	US-10-286-926-27
3	2364	100.0	484	15	US-10-231-913-123
4	2361	99.9	467	15	US-10-231-913-36
5	2357	99.7	484	15	US-10-231-913-124
6	2116	89.5	446	15	US-10-231-913-38
7	2083.5	87.3	455	15	US-10-231-913-125
8	1954	82.7	379	15	US-10-231-913-271
9	1007	42.6	427	15	US-10-231-913-126
10	999	42.3	428	13	US-10-091-085-3
11	999	42.3	428	13	US-10-091-085-5
12	999	42.3	428	13	US-10-092-063-3
13	999	42.3	428	13	US-10-092-063-5

14	999	42.3	428	14	US-10-286-926-3	Sequence 3, Appli
15	999	42.3	428	14	US-10-286-926-5	Sequence 5, Appli
16	999	42.3	428	15	US-10-231-913-127	Sequence 127, App
17	996	42.1	428	13	US-10-091-085-7	Sequence 7, Appli
18	996	42.1	428	13	US-10-092-063-7	Sequence 7, Appli
19	996	42.1	428	14	US-10-286-926-7	Sequence 7, Appli
20	992	42.0	428	16	US-10-408-765A-2296	Sequence 2296, Ap
21	909	38.5	405	13	US-10-092-063-25	Sequence 25, Appl
22	909	38.5	405	14	US-10-286-926-25	Sequence 25, Appl
23	909	38.5	465	13	US-10-092-063-39	Sequence 39, Appl
24	823	34.8	330	9	US-09-925-299-876	Sequence 876, App
25	823	34.8	330	10	US-09-925-299-876	Sequence 876, App
26	590.5	25.0	479	14	US-10-369-493-6447	Sequence 6447, Ap
27	525.5	22.2	467	9	US-09-129-112-19	Sequence 19, Appl
28	508.5	21.5	433	15	US-10-425-114-36762	Sequence 36762, A
29	508	21.5	556	14	US-10-369-493-2169	Sequence 2169, Ap
30	506	21.4	462	9	US-09-129-112-2	Sequence 2, Appli
31	504	21.3	467	15	US-10-425-114-45875	Sequence 45875, A
32	501	21.2	459	9	US-09-129-112-9	Sequence 9, Appli
33	500.5	21.2	562	17	US-10-425-115-334052	Sequence 334052,
34	500	21.2	467	15	US-10-424-599-230158	Sequence 230158,
35	498	21.1	518	14	US-10-369-493-1713	Sequence 1713, Ap
36	491	20.8	534	16	US-10-437-963-132351	Sequence 132351, A
37	490.5	20.7	443	15	US-10-425-114-49933	Sequence 49933, A
38	489	20.7	464	17	US-10-425-115-185050	Sequence 185050,
39	483	20.4	457	15	US-10-425-114-51762	Sequence 51762, A
40	483	20.4	459	15	US-10-424-599-145076	Sequence 145076,
41	478.5	20.2	410	15	US-10-231-913-272	Sequence 272, App
42	467	19.8	469	17	US-10-739-930-10227	Sequence 10227, A
43	463	19.6	462	9	US-09-129-112-15	Sequence 15, Appl
44	452.5	19.1	516	17	US-10-425-115-338300	Sequence 338300,
45	447	18.9	463	17	US-10-425-115-213115	Sequence 213115,

ALIGNMENTS

RESULT 1

US-10-092-063-27

; Sequence 27, Application US/10092063

; Publication No. US20020173005A1

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Mulero, Julio

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES

; FILE REFERENCE: 28110/35908

; CURRENT APPLICATION NUMBER: US/10/092,063

; CURRENT FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: 09/370,265

; PRIOR FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: PCT/US99/16180

; PRIOR FILING DATE: 1999-07-16

; PRIOR APPLICATION NUMBER: 09/350,836

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: 09/273,447

; PRIOR FILING DATE: 1999-03-19

; PRIOR APPLICATION NUMBER: 09/244,444

; PRIOR FILING DATE: 1999-02-04

; PRIOR APPLICATION NUMBER: 09/122,449

; PRIOR FILING DATE: 1998-07-24

; PRIOR APPLICATION NUMBER: 09/118,205

; PRIOR FILING DATE: 1998-07-16

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 484

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-092-063-27

Query Match 100.0%; Score 2364; DB 13; Length 484;
Best Local Similarity 100.0%; Pred. No. 8.7e-218;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 2364; DB 14; Length 484;
Best Local Similarity 100.0%; Pred. No. 8,7e-218;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRKISHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGQOAH 60
DB 29 MRKISHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGQOAH 88
QY 61 SPLGTAAADGHEVYGMFMDAGSTGTRVHVQFTRPPRETPTLTHTETFKAVKPGLSAYADD 120
DB 89 SPLGTAAADGHEVYGMFMDAGSTGTRVHVQFTRPPRETPTLTHTETFKAVKPGLSAYADD 148
QY 121 VEKSAQGIREDLLVAKQDIPDFFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
DB 149 VEKSAQGIREDLLVAKQDIPDFFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208
QY 181 FLVGDDCVSIMGNTDEGVSAWITINFLTGSLKTPGGSSVGMULDGGSGTOIAFLPRVEGT 240
DB 209 FLVGDDCVSIMGNTDEGVSAWITINFLTGSLKTPGGSSVGMULDGGSGTOIAFLPRVEGT 268
QY 241 LQASPPGYLTALRMFNRTYKLYSYSLGLGIMSARLAILGGVEGQPAKDGKELVSPCLSP 300
DB 269 LQASPPGYLTALRMFNRTYKLYSYSLGLGIMSARLAILGGVEGQPAKDGKELVSPCLSP 328
QY 301 SFKGEWEHAEVTVRVSGQKAAASLHELCAARVSEVLQNRVHRTBEVKHVDVFAFSYYIDL 360
DB 329 SFKGEWEHAEVTVRVSGQKAAASLHELCAARVSEVLQNRVHRTBEVKHVDVFAFSYYIDL 388
QY 361 AAGVGLIDAEGKGLSVGVDFEIAAKYVCRTLETOQSSPFCMDLTVVSLLLQBFGRPS 420
DB 389 AAGVGLIDAEGKGLSVGVDFEIAAKYVCRTLETOQSSPFCMDLTVVSLLLQBFGRPS 448
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 456
DB 449 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 484

RESULT 2

US-10-286-926-27
; Sequence 27, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-27

RESULT 3

US-10-231-913-123
; Sequence 123, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderina, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12

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; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-123

Query Match      100.0%; Score 2364; DB 15; Length 484;
Best Local Similarity 100.0%; Pred. No. 8,7e-218;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWGQQA 60
Db 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWGQQA 88

QY 61 SPLGTAADGHEVFYIGIMFDAGSTGTRVHVFOFTPPRETPTLTHTFKAVKPGLSAYADD 120
Db 89 SPLGTAADGHEVFYIGIMFDAGSTGTRVHVFOFTPPRETPTLTHTFKAVKPGLSAYADD 148

QY 121 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
Db 149 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

QY 181 FLVGDDCVSINMGTDGVSAMITINFLTGSUKTPGSSVGMLDLGGGSTQIAFLPRVEGT 240
Db 209 FLVGDDCVSINMGTDGVSAMITINFLTGSUKTPGSSVGMLDLGGGSTQIAFLPRVEGT 268

QY 241 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300
Db 269 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 328

QY 301 SFKGEWEHAETVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDFAFSYYIDL 360
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QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQEGFPFRS 420
Db 389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQEGFPFRS 448

QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
Db 449 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484

RESULT 4
US-10-231-913-36
; Sequence 36, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.

```

```

; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-36

Query Match      99.9%; Score 2361; DB 15; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.6e-217;
Matches 455; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWGQQA 60
Db 12 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWGQQA 71

QY 61 SPLGTAADGHEVFYIGIMFDAGSTGTRVHVFOFTPPRETPTLTHTFKAVKPGLSAYADD 120
Db 72 SPLGTAADGHEVFYIGIMFDAGSTGTRVHVFOFTPPRETPTLTHTFKAVKPGLSAYADD 131

QY 121 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
Db 132 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 191

QY 181 FLVGDDCVSINMGTDGVSAMITINFLTGSUKTPGSSVGMLDLGGGSTQIAFLPRVEGT 240
Db 192 FLVGDDCVSINMGTDGVSAMITINFLTGSUKTPGSSVGMLDLGGGSTQIAFLPRVEGT 251

QY 241 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300
Db 252 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 311

QY 301 SFKGEWEHAETVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDFAFSYYIDL 360
Db 312 SFKGEWEHAETVYRVSGQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDFAFSYYIDL 371

QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQEGFPFRS 420
Db 372 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQEGFPFRS 431

QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456

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Db 432 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 467
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RESULT 5
US-10-231-913-124
; Sequence 124, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 124
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-124
Query Match 99.7%; Score 2357; DB 15; Length 484;
Best Local Similarity 99.6%; Pred. No. 4.1e-217;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKINHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSTTRAPGARWQQA 60
Db 29 MKKINHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSTTRAPGARWQQA 88
QY 61 SPLGTAADGHEVFGYIMFDAGSTGRVHVVFQTRPREPTTLTHETFFKAVKGLSAYADD 120
Db 89 SPLGTAADGHEVFGYIMFDAGSTGRVHVVFQTRPREPTTLTHETFFKAVKGLSAYADD 148
QY 121 VEKSAQGIREDLDVAKQDIPDFFWKATPLVLKATAGRLLLPGEKAQKLLQKVKEFKASP 180
|||||
Db 149 VEKSAQGIREDLDVAKQDIPDFFWKATPLVLKATAGRLLLPGEKAQKLLQKVKEFKASP 208
QY 181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMGLDGGGSGTQIAFLPRVEGT 240
Db 209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMGLDGGGSGTQIAFLPRVEGT 268
QY 241 LQASPPGYLTALRMFNRTYKLYSYVILGGLMSARLAILGGVGGQPAKDKGKELVSPCLSP 300
Db 269 LQASPPGYLTALRMFNRTYKLYSYVILGGLMSARLAILGGVGGQPAKDKGKELVSPCLSP 328
QY 301 SPKGEWEHAEVTVYRVSQKAAASLHELCAARVSEVLQNRVHRTEEVKXVDFYAFSYYIDL 360
Db 329 SPKGEWEHAEVTVYRVSQKAAASLHELCAARVSEVLQNRVHRTEEVKXVDFYAFSYYIDL 388
QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRLETQPOSSPFCMDLTVVSLLLQEFQPPRS 420
Db 389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRLETQPOSSPFCMDLTVVSLLLQEFQPPRS 448
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
Db 449 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
|||||
RESULT 6
US-10-231-913-38
; Sequence 38, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-38

Query Match      89.5%; Score 2116; DB 15; Length 446;
Best Local Similarity 91.0%; Pred. No. 5.1e-194;
Matches 415; Conservative 1; Mismatches 2; Indels 38; Gaps 1;

QY      1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQAAH 60
Db      29 MRKISNHGSLRVAV-----ARWQQAAH 50

QY      61 SPLGTAADGHEVYFGIMFDAGSTGTRVHVFOFTRPPRETPTLTHETFKAVKGLSAYADD 120
Db      51 SPLGTAADGHEVYFGIMFDAGSTGTRVHVFOFTRPPRETPTLTHETFKALKPLGSAYADD 110

QY      121 VEKSAQGIREDLVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP 180
Db      111 VEKSAQGIREDLVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP 170

QY      181 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGSSVGMDLGGGSTQIAFLPRVEGT 240
Db      171 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGSSVGMDLGGGSTQIAFLPRVEGT 230

QY      241 LQASPPGYLTALRMFNRTYKLYSYSLGLGMSARLAILGGVGGOPAKDGKELVSPCLSP 300
Db      231 LQASPPGYLTALRMFNRTYKLYSYSLGLGMSARLAILGGVGGOPAKDGKELVSPCLSP 290

QY      301 SPFGWEHAETVRYVSGGKAAASLHELCAARVSEVLQNRVHRTVEVKHVDVFAYFSYYDL 360
Db      291 SPFGWEHAETVRYVSGGKAAASLHELCAARVSEVLQNRVHRTVEVKHVDVFAYFSYYDL 350

QY      361 AAGVGLIDAEGKGLVVDGDFEIAAKYVCRTELTQPSPPSCMDLTYVSLLLQEFGFPFRS 420
Db      351 AAGVGLIDAEGKGLVVDGDFEIAAKYVCRTELTQPSPPSCMDLTYVSLLLQEFGFPFRS 410

QY      421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 456
Db      411 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 446

RESULT 7
US-10-231-913-125
; Sequence 125, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zernusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
```

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; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-231-913-125

Query Match      87.3%; Score 2063.5; DB 15; Length 455;
Best Local Similarity 86.6%; Pred. No. 5.7e-189;
Matches 394; Conservative 27; Mismatches 33; Indels 1; Gaps 1;

QY      1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQAAH 60
Db      1 MRKIPNHGTLRMKTVAYPLGLCVGLFIYVAYIKWRASAAQAFFIAGAAAGVVRWTQQA 60

QY      61 SPLGTAADGHEVYFGIMFDAGSTGTRVHVFOFTRPPRETPTLTHETFKAVKGLSAYADD 120
Db      61 SSPDATRGHEVYFGIMFDAGSTGTRVHVFOFTRPPRETPTLTHETFKALKPLGSAYADD 120

QY      121 VEKSAQGIREDLVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP 180
Db      121 VEKSAQGIREDLVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP 180

QY      181 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGSSVGMDLGGGSTQIAFLPRVEGT 240
Db      181 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGSSVGMDLGGGSTQITFLPRVEGT 240

QY      241 LQASPPGYLTALRMFNRTYKLYSYSLGLGMSARLAILGGVGGOPAKDGKELVSPCLSP 300
Db      241 LQASPPGYLTALRMFNRTYKLYSYSLGLGMSARLAILGGVGGOPAKDGKELVSPCLSP 300

QY      301 SPFGWEHAETVRYVSGGKAAASLHELCAARVSEVLQNRVHRTVEVKHVDVFAYFSYYDL 360
Db      301 RFRGWEHAETVRYISGOK-AVGLVELCASRVSEVLNRKVRHRTVEAQHVDFYAFSYYDL 359

QY      361 AAGVGLIDAEGKGLVVDGDFEIAAKYVCRTELTQPSPPSCMDLTYVSLLLQEFGFPFRS 420
Db      360 AASFGLIDAEGKGLVVDGDFEIAAKYVCRTELTQPSPPSCMDLTYVSLLLHFEFGFPGD 419

QY      421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPA 455
Db      420 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPA 454

RESULT 8
US-10-231-913-271
; Sequence 271, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
```

APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Vernet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eisen, Andrew J.
APPLICANT: Liu, Xiaohong
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 271
LENGTH: 379
TYPE: PRT
ORGANISM: Homo sapiens
US-10-231-913-271
Query Match 82.7%; Score 1954; DB 15; Length 379;
Best Local Similarity 99.7%; Pred. No. 1.4e-178;
Matches 378; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 71 EVFYGMFDAGSTGRVHVFOFTRPREPTLTHTETKAVKPGLSAYADDDVEKSAQGIRE 130
DB 1 EVFYGMFDAGSTGRVHVFOFTRPREPTLTHTETKAVKPGLSAYADDDVEKSAQGIRE 60
QY 131 LLDVAKQDIPDFWKATPLVLKATAGLLPGEKAQKLLQKVEFKASPFVLVGDCVSI 190
DB 61 LLDVAKQDIPDFWKATPLVLKATAGLLPGEKAQKLLQKVEFKASPFVLVGDCVSI 120
QY 191 NNGTDEGVSANITINFLGSLKTPGSSVGMJDLGGSGTQIAFLPRVEGTLOASPPGYLT 250
DB 121 NNGTDEGVSANITINFLGSLKTPGSSVGMJDLGGSGTQIAFLPRVEGTLOASPPGYLT 180
QY 251 ALRMENRTKLYSYGLGMSARIALILGGVEGQPAKDGKELVSPCLSPSPKGEWEHAE 310
DB 181 ALRMENRTKLYSYGLGMSARIALILGGVEGQPAKDGKELVSPCLSPSPKGEWEHAE 240
QY 311 VTYRVSGQKAASLHELCAARVSEVLQNRVHRTTEEVKHVDFYAFSYIIDLAAGVGLIDAE 370
DB 241 VTYRVSGQKAASLHELCAARVSEVLQNRVHRTTEEVKHVDFYAFSYIIDLAAGVGLIDAE 300
QY 371 KGSILVVGDFEIAAKVVCRTLETQPOSSPFCMDLTIVSVLLQLQBFGRPSKVLKLTREKID 430

Db 301 KGSILVVGDFEIAAKVVCRTLETQPOSSPFCMDLTIVSVLLQLQBFGRPSKVLKLTREKID 360
QY 431 NVETSWALGAIFHYIDSLN 449
Db 361 NVETSWALGAIFHYIDSLN 379
RESULT 9
US-10-231-913-126
Sequence 126, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Vernet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eisen, Andrew J.
APPLICANT: Liu, Xiaohong
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 126
LENGTH: 427
TYPE: PRT
ORGANISM: Mus musculus
US-10-231-913-126
Query Match 42.6%; Score 1007; DB 15; Length 427;
Best Local Similarity 50.0%; Pred. No. 1.5e-87;
Matches 213; Conservative 62; Mismatches 133; Indels 18; Gaps 6;
QY 37 ATATQAQFSITPAARCA-----RWGQ-----QAHSPGLGTAAAGHVEFYGMFDAGSTG 84
DB 2 ATSWGAFMLIITACVGVTFVREQQTWFEVFLSSMCPINVSAG---TFYGMFDAGSTG 58
QY 85 TTVHVFOFQFT-RPREPTLTHTETKAVKPGLSAYADDDVEKSAQGIREDLVAKQDIPDF 143

Db 59 TRIHVTVFVKTAGQLPFFLEGEIFDVSXPKLSAFVDPKQGAETVQELLEVAKDSIPRGH 118
QY 144 WKATPLVLKATAGRLLPCKEAKQLQKVEKVFKAPELVGDDCVSMNGTDEGVSAWIT 203
Db 119 WERTPVVLKATAGRLLPCKEAKQLLEVEIFKNSFFLVPGSVSMDGSEYEGILAWVT 178
QY 204 INFLTGLSKTPGSSVGMLDLGGSTQIAFLPRVECTLOASPPGYLTALRMFNRTYKLYS 263
Db 179 VNFLTQGLHGRGQETVGTLDGGASTQITFLPQFKTLEQTGRGYLTSTFEMFNSTFKLYT 238
QY 264 YSYLGLGLMSARLAILGGVGGOPAKDKELVSPCLSPSPFKGEWHAETVRYVSGQKAAAS 323
Db 239 HGSLFGGLKAARLAILGALAEK-GTGDGTFRACLPRLWEAEWIFGVGVYQYCGNQEGEM 297
QY 324 LHELCAARVSEVLQNRVHRTTEEVKHVDYAFVSYYYDLAAGVGLIDAEGKGSVWGDFFETA 383
Db 298 GFEPCEAEVLRVVQGLKHQPEEVRGSAFAYFYVYDRAADTHLIDYEKGGLVKVEDFERK 357
QY 384 AKYVCRTLETQSQSPFSCMDLTYVSLLOE-FGPPRSKVLKTRKIDNVETSWALGAIF 442
Db 358 AREVCDNLGSSGSPFLCMLDLYTALLKDGFGFADGTLQLTKVNNIETGVALGATF 417
QY 443 HYDLSL 448
Db 418 HLLQSL 423

RESULT 10
US-10-091-085-3
; Sequence 3, Application US/10091085
; Publication No. US20020146772A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/10/091,085
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-085-3

Query Match 42.3%; Score 999; DB 13; Length 428;
Best Local Similarity 52.4%; Pred. No. 8.8e-87;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

QY 62 PLGTAADGHEVYFYMFDAGSTGTRVHVFOFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
Db 40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGOLPILEGEVDFSVKPGLSAFVDQ 96
QY 121 VEKSAOGTRELIDVAKQDIPDFWKATPLVLKATAGRLLLPCKEAKQLQKVEVFKASP 180
Db 97 PKQGAETVQGLLEVAKOSIPRSHWKKTPVLKATAGRLLLPEHAKALLFEVKEIFRKPSP 156
QY 181 FLVGDDCVSMNGTDEGVSAWITINFLTGLSKTPGSSVGMLDLGGSTQIAFLPRVEGT 240
Db 157 FLVFKGVSIMDGSEGLAWVTNFLTGLQHGRQETVGTLDLGGASTQITFLPQFEKT 216
QY 241 LOASPPGYLTALRMFNRTYKLYSYSLGLGLMSARLAILGGVGGOPAKDKGKELVSPCLSP 300
Db 217 LEQTPRGYLTSTFEMFNSTFKLYTHSYLGFGLKAARLAILGALAEK-GTGDGTFRACLP 275
QY 301 SPKGEWHAETVRYVSGQKAAASLHELCAARVSEVLQNRVHRTTEEVKHVDYAFVSYYYDL 360
Db 276 WLEAEWIFGVGVYQYCGNQEGEVGFEPCYAEVLRVVRGKLHQPPEVQSGSFYAFSYYDR 335
QY 361 AAGVGLIDAEGKGSVWGDFFETAAYVCRILETQPSQSPFSCMDLTYVSLLOE-FGPPR 419

QY 241 LOASPPGYLTALRMFNRTYKLYSYSLGLGLMSARLAILGGVGGOPAKDKGKELVSPCLSP 300
Db 217 LEQTPRGYLTSTFEMFNSTFKLYTHSYLGFGLKAARLAILGALAEK-GTGDGTFRACLP 275
QY 301 SPKGEWHAETVRYVSGQKAAASLHELCAARVSEVLQNRVHRTTEEVKHVDYAFVSYYYDL 360
Db 276 WLEAEWIFGVGVYQYCGNQEGEVGFEPCYAEVLRVVRGKLHQPPEVQSGSFYAFSYYDR 335
QY 361 AAGVGLIDAEGKGSVWGDFFETAAYVCRILETQPSQSPFSCMDLTYVSLLOE-FGPPR 419
Db 236 AYDTMDIDYKGGILKVEDFERKAREVCNLENFTSGSPFLCMLDLYTALLKDGFGFAD 395
QY 420 SKVLKTRKIDNVETSWALGAIFHYDLSL 448
Db 396 STVLQUTTKVNNIETGVALGATFHLQSL 424

RESULT 11
US-10-091-085-5
; Sequence 5, Application US/10091085
; Publication No. US20020146772A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/10/091,085
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-085-5

Query Match 42.3%; Score 999; DB 13; Length 428;
Best Local Similarity 52.4%; Pred. No. 8.8e-87;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

QY 62 PLGTAADGHEVYFYMFDAGSTGTRVHVFOFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
Db 40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGOLPILEGEVDFSVKPGLSAFVDQ 96
QY 121 VEKSAOGTRELIDVAKQDIPDFWKATPLVLKATAGRLLLPCKEAKQLQKVEVFKASP 180
Db 97 PKQGAETVQGLLEVAKOSIPRSHWKKTPVLKATAGRLLLPEHAKALLFEVKEIFRKPSP 156
QY 181 FLVGDDCVSMNGTDEGVSAWITINFLTGLSKTPGSSVGMLDLGGSTQIAFLPRVEGT 240
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QY 361 AAGVGLIDAEGKGSVWGDFFETAAYVCRILETQPSQSPFSCMDLTYVSLLOE-FGPPR 419


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; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
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; TITLE OF INVENTION: Polypeptides
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; FILE REFERENCE: 28110/36457CON
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; CURRENT APPLICATION NUMBER: US/10/286,926
;
; CURRENT FILING DATE: 2002-11-01
;
; PRIOR APPLICATION NUMBER: 09/557,800
;
; PRIOR FILING DATE: 2000-04-25
;
; PRIOR APPLICATION NUMBER: 09/481,238
;
; PRIOR FILING DATE: 2000-01-11
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; PRIOR APPLICATION NUMBER: 09/370,265
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; PRIOR FILING DATE: 1999-08-09
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; PRIOR APPLICATION NUMBER: PCT/US99/16180
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; PRIOR FILING DATE: 1999-07-16
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; PRIOR APPLICATION NUMBER: 09/350836
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; PRIOR FILING DATE: 1999-07-09
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; PRIOR APPLICATION NUMBER: 09/273447
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; PRIOR FILING DATE: 1999-03-19
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; PRIOR APPLICATION NUMBER: 09/122449
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; PRIOR FILING DATE: 1998-07-24
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; PRIOR APPLICATION NUMBER: 09/244444
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; PRIOR FILING DATE: 1999-02-04
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; PRIOR APPLICATION NUMBER: 09/118,205
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; PRIOR FILING DATE: 1998-07-16
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; NUMBER OF SEQ ID NOS: 54
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; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 5
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; LENGTH: 428
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; TYPE: PRT
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; ORGANISM: Homo sapiens
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; US-10-286-926-5

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Query Match	42.38;	Score	999;	DB	14;	Length	428;
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QY	241	LQASPPGYLTALRMFNRTKLYXSYSYGLGLGIMARLAILGVEGQPAKDQKELVSPCLSP	300				
Db	217	LEQTPRGYLTSPWFENSTYKLYTHSYLGFGLKAARLATALGALETE-CTDGHFTFSACLPR	275				
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QY	361	ACAGVLIDAEKGSVLVVGDFEIAAKVYCRTRLETQPOSSPFSCMDLTVVSLLLQE-FGFPR	419				
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Search completed: November 16, 2004, 17:12:01
Job time : 144 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 16:38:51 ; Search time 40 Seconds
(without alignments)
756.025 Million cell updates/sec

Title: US-09-905-589A-2

Perfect score: 2364

Sequence: 1 MRKISNHGSLRVAKVAYPLG.....ALGAIFHYDLSNRKQSPAS 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2364	100.0	456	US-09-240-639-2	Sequence 2, Appli
2	2364	100.0	456	US-09-908-510A-2	Sequence 2, Appli
3	2364	100.0	456	US-09-905-744-2	Sequence 2, Appli
4	2364	100.0	456	US-10-107-660-2	Sequence 2, Appli
5	2364	100.0	456	US-10-107-576-2	Sequence 2, Appli
6	2364	100.0	456	US-09-905-732-2	Sequence 2, Appli
7	2364	100.0	484	US-09-608-285A-27	Sequence 27, Appl
8	2364	100.0	484	US-09-370-265-27	Sequence 27, Appl
9	2364	100.0	484	US-09-557-800C-27	Sequence 27, Appl
10	2364	100.0	484	US-09-370-625A-27	Sequence 27, Appl
11	2003	84.7	471	US-09-608-285A-60	Sequence 60, Appl
12	999	42.3	428	US-09-608-285A-3	Sequence 3, Appli
13	999	42.3	428	US-09-608-285A-5	Sequence 5, Appli
14	999	42.3	428	US-09-240-639-6	Sequence 6, Appli
15	999	42.3	428	US-09-240-639-9	Sequence 9, Appli
16	999	42.3	428	US-09-350-836B-3	Sequence 3, Appli
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31	999	42.3	428	4	US-10-107-576-9	Sequence 9, Appli
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34	996	42.1	428	3	US-09-608-285A-7	Sequence 7, Appli
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39	909	38.5	405	3	US-09-608-285A-25	Sequence 25, Appl
40	909	38.5	405	4	US-09-370-265-25	Sequence 25, Appl
41	909	38.5	405	4	US-09-557-800C-25	Sequence 25, Appl
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43	909	38.5	465	4	US-09-557-800C-56	Sequence 56, Appl
44	909	38.5	465	4	US-09-370-625A-39	Sequence 39, Appl
45	904	38.2	465	3	US-09-240-639-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-639-2
; Sequence 2, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-2

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US-09-908-510A-2
; Sequence 2, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-908-510A-2
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Best Local Similarity 100.0%; Pred. No. 1.1e-230;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 2, Application US/09905744
; Patent No. 6780410
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/10/107,660
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-660-2

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/905,744
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-744-2
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Best Local Similarity 100.0%; Pred. No. 1.1e-230;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-107-660-2
; Sequence 2, Application US/10107660
; Patent No. 6780977
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/10/107,660
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-660-2

Query Match 100.0%; Score 2364; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.1e-230;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-107-576-2
; Sequence 2, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/10/107,576
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-576-2

Query Match 100.0%; Score 2364; DB 4; Length 456;
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Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 AAGVGLIDAEGKGSLLVVGDFEIAAKYVCRITLETQPSPPSCMDLTVVSLLLQEGFGPRS 420

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Db 421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 456

RESULT 6
US-09-905-732-2
; Sequence 2, Application US/09905732
; Patent No. 6787328
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/905,732
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-732-2

Query Match 100.0%; Score 2364; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.1e-230;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGQOAH 60
Db 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFPSITRAAPGARWGQOAH 60

QY 61 SPLGTAADGHEVFYIGIMFDAGSTGRVHVVFQTRPPRETPTLTHTETFAKVPGLSAYADD 120
Db 61 SPLGTAADGHEVFYIGIMFDAGSTGRVHVVFQTRPPRETPTLTHTETFAKVPGLSAYADD 120

QY 121 VEKSAQGIREDLDVAKQDIPDFWKAATPLVLKATAGRLLLPGEKAQKLLQKVKEVFKASP 180
Db 121 VEKSAQGIREDLDVAKQDIPDFWKAATPLVLKATAGRLLLPGEKAQKLLQKVKEVFKASP 180

QY 181 FLVGDDCVSIMNGTDEGVSAMITINFLTGSILKTPGGSSVGMLDLGGGSGTQIAFLPRVEGT 240
Db 181 FLVGDDCVSIMNGTDEGVSAMITINFLTGSILKTPGGSSVGMLDLGGGSGTQIAFLPRVEGT 240

QY 241 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300
Db 241 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVEGQPAKDGKELVSPCLSP 300

QY 301 SPKGWEHAETVRYVSGQKAAASLHELCAARVSEVLQNRVHRTTEVKHVDYFAFSYYIDL 360
Db 301 SPKGWEHAETVRYVSGQKAAASLHELCAARVSEVLQNRVHRTTEVKHVDYFAFSYYIDL 360

QY 361 AAGVGLIDAEGKGSLLVVGDFEIAAKYVCRITLETQPSPPSCMDLTVVSLLLQEGFGPRS 420
Db 361 AAGVGLIDAEGKGSLLVVGDFEIAAKYVCRITLETQPSPPSCMDLTVVSLLLQEGFGPRS 420

QY 421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 456
Db 421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 456

QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTELETOPOSSPFCMDLTYSVLLQLQFPGPSP 420
Db 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTELETOPOSSPFCMDLTYSVLLQLQFPGPSP 420
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 456
Db 421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 456

RESULT 7

US-09-608-285A-27
; Sequence 27, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-27

Query Match 100.0%; Score 2364; DB 3; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.2e-230; Mismatches 0; Indels 0; Gaps 0;
Matches 456; Conservative 0;
QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQA 60
Db 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQA 88
QY 61 SPLGTAADGHEVFGYIMFDAGSTGTRVHVQFTRPPRETPTLTHTFKAVKPGLSAYADD 120
Db 89 SPLGTAADGHEVFGYIMFDAGSTGTRVHVQFTRPPRETPTLTHTFKAVKPGLSAYADD 148
QY 121 VEKSAQGRRELDVAKQDIPDFWKATPLVLKATAGLLPCKEAKLLQKVKEVFKASP 180
Db 149 VEKSAQGRRELDVAKQDIPDFWKATPLVLKATAGLLPCKEAKLLQKVKEVFKASP 208
QY 181 FLVGGDCVSIIMGTDGVSAMITINFLTGLSKTPGSSVGMLDLGGSGTQIAFLPRVEGT 240
Db 209 FLVGGDCVSIIMGTDGVSAMITINFLTGLSKTPGSSVGMLDLGGSGTQIAFLPRVEGT 268
QY 241 LOASPPGYLTALRMENRTYKLYSYLGLGMSARLAILGGVEGQPAKDKELVSPCLSP 300
Db 269 FLVGGDCVSIIMGTDGVSAMITINFLTGLSKTPGSSVGMLDLGGSGTQIAFLPRVEGT 268
QY 241 LOASPPGYLTALRMENRTYKLYSYLGLGMSARLAILGGVEGQPAKDKELVSPCLSP 300

Db 269 LOASPPGYLTALRMENRTYKLYSYLGLGMSARLAILGGVEGQPAKDKELVSPCLSP 328
QY 301 SFKGWEHAEVTVRVSGQKAAASLHELCAARVSVLQNRVHRTVEVKHVDYFAFSYYIDL 360
Db 329 SFKGWEHAEVTVRVSGQKAAASLHELCAARVSVLQNRVHRTVEVKHVDYFAFSYYIDL 388
QY 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTELETOPOSSPFCMDLTYSVLLQLQFPGPSP 420
Db 389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTELETOPOSSPFCMDLTYSVLLQLQFPGPSP 448
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 456
Db 449 KVLKTRKIDNVETSWALGAIFHYIDSINRQKSPAS 484

RESULT 8

US-09-370-265-27
; Sequence 27, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-27

Query Match 100.0%; Score 2364; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.2e-230; Mismatches 0; Indels 0; Gaps 0;
Matches 456; Conservative 0;
QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQA 60
Db 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQA 88
QY 61 SPLGTAADGHEVFGYIMFDAGSTGTRVHVQFTRPPRETPTLTHTFKAVKPGLSAYADD 120
Db 89 SPLGTAADGHEVFGYIMFDAGSTGTRVHVQFTRPPRETPTLTHTFKAVKPGLSAYADD 148
QY 121 VEKSAQGRRELDVAKQDIPDFWKATPLVLKATAGLLPCKEAKLLQKVKEVFKASP 180
Db 149 VEKSAQGRRELDVAKQDIPDFWKATPLVLKATAGLLPCKEAKLLQKVKEVFKASP 208
QY 181 FLVGGDCVSIIMGTDGVSAMITINFLTGLSKTPGSSVGMLDLGGSGTQIAFLPRVEGT 240
Db 209 FLVGGDCVSIIMGTDGVSAMITINFLTGLSKTPGSSVGMLDLGGSGTQIAFLPRVEGT 268
QY 241 LOASPPGYLTALRMENRTYKLYSYLGLGMSARLAILGGVEGQPAKDKELVSPCLSP 300
Db 269 LOASPPGYLTALRMENRTYKLYSYLGLGMSARLAILGGVEGQPAKDKELVSPCLSP 328
QY 301 SFKGWEHAEVTVRVSGQKAAASLHELCAARVSVLQNRVHRTVEVKHVDYFAFSYYIDL 360

Db 329 SFKGEWHAETVYRVSGKAAASLHELCAARVSEVLQNRVHRTTEVKHVDYFAFSYYDL 388
QY 361 AAGVGLIDAEGKGSLLVGDFFETAAKYVCTLTETQSSPFCMDLTYVSLLLQEGFPPRS 420
Db 389 AAGVGLIDAEGKGSLLVGDFFETAAKYVCTLTETQSSPFCMDLTYVSLLLQEGFPPRS 448
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
Db 449 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484

RESULT 9

US-09-557-800C-27
; Sequence 27, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350936
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-27

Query Match 100.0%; Score 2364; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.2e-230;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAVIKWHRATATQAFSITRAAPGARWQQA 60
Db 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAVIKWHRATATQAFSITRAAPGARWQQA 88
QY 61 SPLGTADGHEVYFGIMPDAGSTGRVHVFOFTPRPTTLTHTETFAKVPGLSAYADD 120
Db 89 SPLGTADGHEVYFGIMPDAGSTGRVHVFOFTPRPTTLTHTETFAKVPGLSAYADD 148
QY 121 VEKSAQGIREDLLDVAQDIPDFWKATPLVLKATAGLLPGEKAQKLLQKVKEVFKASP 180
Db 149 VEKSAQGIREDLLDVAQDIPDFWKATPLVLKATAGLLPGEKAQKLLQKVKEVFKASP 208
QY 181 FLVGDDCVSINMGTDGVSAMITINFLTGSLKTPGSSVGMLDLGGSGTQIAFLPRVEGT 240
Db 209 FLVGDDCVSINMGTDGVSAMITINFLTGSLKTPGSSVGMLDLGGSGTQIAFLPRVEGT 268
QY 241 LQASPPGYLTALRMFNRTYKLYSYSLGLGLMSARLAILGGVEGOPAKDGKELVSPCLSP 300
Db 269 LQASPPGYLTALRMFNRTYKLYSYSLGLGLMSARLAILGGVEGOPAKDGKELVSPCLSP 328
QY 301 SFKGEWHAETVYRVSGKAAASLHELCAARVSEVLQNRVHRTTEVKHVDYFAFSYYDL 360
Db 329 SFKGEWHAETVYRVSGKAAASLHELCAARVSEVLQNRVHRTTEVKHVDYFAFSYYDL 388
QY 361 AAGVGLIDAEGKGSLLVGDFFETAAKYVCTLTETQSSPFCMDLTYVSLLLQEGFPPRS 420
Db 389 AAGVGLIDAEGKGSLLVGDFFETAAKYVCTLTETQSSPFCMDLTYVSLLLQEGFPPRS 448
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
Db 449 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484

Db 329 SFKGEWHAETVYRVSGKAAASLHELCAARVSEVLQNRVHRTTEVKHVDYFAFSYYDL 388
QY 361 AAGVGLIDAEGKGSLLVGDFFETAAKYVCTLTETQSSPFCMDLTYVSLLLQEGFPPRS 420
Db 389 AAGVGLIDAEGKGSLLVGDFFETAAKYVCTLTETQSSPFCMDLTYVSLLLQEGFPPRS 448
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
Db 449 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484

RESULT 10

US-09-370-625A-27
; Sequence 27, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-625A-27

Query Match 100.0%; Score 2364; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.2e-230;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAVIKWHRATATQAFSITRAAPGARWQQA 60
Db 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAVIKWHRATATQAFSITRAAPGARWQQA 88
QY 61 SPLGTADGHEVYFGIMPDAGSTGRVHVFOFTPRPTTLTHTETFAKVPGLSAYADD 120
Db 89 SPLGTADGHEVYFGIMPDAGSTGRVHVFOFTPRPTTLTHTETFAKVPGLSAYADD 148
QY 121 VEKSAQGIREDLLDVAQDIPDFWKATPLVLKATAGLLPGEKAQKLLQKVKEVFKASP 180
Db 149 VEKSAQGIREDLLDVAQDIPDFWKATPLVLKATAGLLPGEKAQKLLQKVKEVFKASP 208
QY 181 FLVGDDCVSINMGTDGVSAMITINFLTGSLKTPGSSVGMLDLGGSGTQIAFLPRVEGT 240
Db 209 FLVGDDCVSINMGTDGVSAMITINFLTGSLKTPGSSVGMLDLGGSGTQIAFLPRVEGT 268
QY 241 LQASPPGYLTALRMFNRTYKLYSYSLGLGLMSARLAILGGVEGOPAKDGKELVSPCLSP 300
Db 269 LQASPPGYLTALRMFNRTYKLYSYSLGLGLMSARLAILGGVEGOPAKDGKELVSPCLSP 328
QY 301 SFKGEWHAETVYRVSGKAAASLHELCAARVSEVLQNRVHRTTEVKHVDYFAFSYYDL 360
Db 329 SFKGEWHAETVYRVSGKAAASLHELCAARVSEVLQNRVHRTTEVKHVDYFAFSYYDL 388
QY 361 AAGVGLIDAEGKGSLLVGDFFETAAKYVCTLTETQSSPFCMDLTYVSLLLQEGFPPRS 420
Db 389 AAGVGLIDAEGKGSLLVGDFFETAAKYVCTLTETQSSPFCMDLTYVSLLLQEGFPPRS 448
QY 421 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
Db 449 KVLKTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484

RESULT 11

US-09-608-285A-60
; Sequence 60, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-60

Query Match 84.7%; Score 2003; DB 3; Length 471;
Best Local Similarity 98.5%; Pred. No. 4.6e-194;
Matches 388; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy	1	MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQA	60
Db	29	MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFSITRAAPGARWQQA	88
Qy	61	SPLGTAADGHEVFGIMFDAGSTGTRVHVFOFTPRPTPTLTTHETFKAVKPGLSAYADD	120
Db	89	SPLGTAADGHEVFGIMFDAGSTGTRVHVFOFTPRPTPTLTTHETFKAVKPGLSAYADD	148
Qy	121	VEKSAQGIREDLLVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP	180
Db	149	VEKSAQGIREDLLVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP	208
Qy	181	FLVGGDDCVSINMGTDGVSAMITINFLTGSLSKTPGSSVGMMLDLGGSGTQIAFLPRVGT	240
Db	209	FLVGGDDCVSINMGTDGVSAMITINFLTGSLSKTPGSSVGMMLDLGGSGTQIAFLPRVGT	268
Qy	241	LOASPPGYLTALRMFNRTYKLYSYLGLGLMSARLAILGGVGGOPAKDGKELVSPCLSP	300
Db	269	LOASPPGYLTALRMFNRTYKLYSYLGLGLMSARLAILGGVGGOPAKDGKELVSPCLSP	328
Qy	301	SPFGWEHAEVTRYVSGQKAAASLHELCAARVSEVLQNRVHRTTEVKHVDVFAFSYYDL	360
Db	329	SPFGWEHAEVTRYVSGQKAAASLHELCAARVSEVLQNRVHRTTEVKHVDVFAFSYYDL	388
Qy	361	AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQ	394
Db	389	AAGVGLIDAEKGGSLVVGDFEIAAKYVGSGLERE	422

RESULT 12

US-09-608-285A-3
; Sequence 3, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-3

Query Match 42.3%; Score 999; DB 3; Length 428;
Best Local Similarity 52.4%; Pred. No. 2.2e-92;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

Qy	62	PLGTAADGHEVFGIMFDAGSTGTRVHVFOFT--PPRETPTLTTHETFKAVKPGLSAYADD	120
Db	40	PINVSAAA--STLYGIMFDAGSTGTRIHVITTVQXMPGQLPILGEVDFSVKPGLSAFVDQ	96
Qy	121	VEKSAQGIREDLLVAKQDIPDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP	180
Db	97	PKQGAETVQGLLEVAKQDIPRSHWKTTPVLKATAGLRLPGEKAQKLLQKVKEVFKASP	156
Qy	181	FLVGGDDCVSINMGTDGVSAMITINFLTGSLSKTPGSSVGMMLDLGGSGTQIAFLPRVGT	240
Db	157	FLVFKGVSINMGDSDEGLAWTVNFLTQGLHGRQETVGTGLDGGASTQITFLPQFBKT	216
Qy	241	LOASPPGYLTALRMFNRTYKLYSYLGLGLMSARLAILGGVGGOPAKDGKELVSPCLSP	300
Db	217	LEQTPRGVLTSEFMFNSTYKLYTHSYLGLGKARLALGALETE-GTDGHTFRSACLPR	275
Qy	301	SPFGWEHAEVTRYVSGQKAAASLHELCAARVSEVLQNRVHRTTEVKHVDVFAFSYYDL	360
Db	276	WLEAEWIFGGVKYQYCGNOEGEVGPEPCYAEVLRVVRGKJHQPEEVQVQSGSFYAFSYYDR	335
Qy	361	AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQ--SSPSCMDLTYSLLLOE-FGPR	419
Db	336	AVDTMDIYEGGILKVEDFERKAREVCNLENFTSGSFLLCMLDLSYITALLKQGGFGAD	395
Qy	420	SKVLKLTAKIDNVETSWALGAIFHYIDSL	448

Db 396 STVQLTKKVNNIETGALGATFHLLQSL 424

RESULT 13
US-09-608-285A-5
; Sequence 5, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-5

Query Match 42.3%; Score 999; DB 3; Length 428;
Best Local Similarity 52.4%; Pred. No. 2.2e-92;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;
Qy 62 PLGTAADGHEVYFYGIMFDAGSTGTRVHVQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
Db 40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDVSVKPGLSAFVDQ 96
Qy 121 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLLPGEKAKQLLKQKVEVFKASP 180
Db 97 PKQGAETVQGLEVAKOSIPRSHWKKTPVLKATAGLRLLPGEKAKALLFEVKEIFRKSP 156
Qy 181 FLVGDDCVSINMGTDGVSAMTINFLTGSLKTPGSSVGMFLDGGSTQIAFLPRVEGT 240
Db 157 FLVPGKGSVIMDGDEGILAWTVNFLTQGLHGRQETVGTLDLGGASTQTTFUPQFEXT 216
Qy 241 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVGGOPAKDGKELVSPCLSP 300
Db 217 LEQTPRGYLTSEFENSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275
Qy 301 SFKEWEHAEVTVYRVSQKAAASHLHCAARVSEVLQNRVHRTBEVKHVDVFAFSYYIDL 360
Db 276 WLEAEWIFGGVKYQYGGNQEVEGPEPCYAEVLRVVRGKLHQPEVQSGSFYAFSYYIDR 335
Qy 361 AAGVGLIDAEGKGLVVGDFEIAAKYVCRTLETQPSPPSCMDLTYYVSLLOE-FGPPR 419
Db 336 AVDTMDIDYEKGGLIKVEDFERKAREVCNDLENFTSGSPFLCNDLSYITALLKOGFGPAD 395
Qy 420 SKVLKLRKIDNVETSWALGAIFHYDLSL 448

Db 396 STVQLTKKVNNIETGALGATFHLLQSL 424

RESULT 14
US-09-240-639-6
; Sequence 6, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-6

Query Match 42.3%; Score 999; DB 3; Length 428;
Best Local Similarity 52.4%; Pred. No. 2.2e-92;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;
Qy 62 PLGTAADGHEVYFYGIMFDAGSTGTRVHVQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
Db 40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDVSVKPGLSAFVDQ 96
Qy 121 VEKSAQGIREDLDVAKQDIPDFWKATPLVLKATAGLRLLPGEKAKQLLKQKVEVFKASP 180
Db 97 PKQGAETVQGLEVAKOSIPRSHWKKTPVLKATAGLRLLPGEKAKALLFEVKEIFRKSP 156
Qy 181 FLVGDDCVSINMGTDGVSAMTINFLTGSLKTPGSSVGMFLDGGSTQIAFLPRVEGT 240
Db 157 FLVPGKGSVIMDGDEGILAWTVNFLTQGLHGRQETVGTLDLGGASTQTTFUPQFEXT 216
Qy 241 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLAILGGVGGOPAKDGKELVSPCLSP 300
Db 217 LEQTPRGYLTSEFENSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275
Qy 301 SFKEWEHAEVTVYRVSQKAAASHLHCAARVSEVLQNRVHRTBEVKHVDVFAFSYYIDL 360
Db 276 WLEAEWIFGGVKYQYGGNQEVEGPEPCYAEVLRVVRGKLHQPEVQSGSFYAFSYYIDR 335
Qy 361 AAGVGLIDAEGKGLVVGDFEIAAKYVCRTLETQPSPPSCMDLTYYVSLLOE-FGPPR 419
Db 336 AVDTMDIDYEKGGLIKVEDFERKAREVCNDLENFTSGSPFLCNDLSYITALLKOGFGPAD 395
Qy 420 SKVLKLRKIDNVETSWALGAIFHYDLSL 448
Db 396 STVQLTKKVNNIETGALGATFHLLQSL 424

RESULT 15
US-09-240-639-9
; Sequence 9, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 428

